

P10161

F-NT2RP2003383

LONG NEUROTOXIN 2 (TOXINS I AND V).

0.86:38:39

DENDROASPIS VIRIDIS (WESTERN GREEN MAMBA).

P01395

F-NT2RP2003390

NPL1 PROTEIN (SEC63 PROTEIN).

1.1e-14:113:38

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P14906

F-NT2RP2003469

MYO-INOSITOL TRANSPORTER 2.

1.7e-09:148:28

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P30606

F-NT2RP2003545

SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).

9.2e-32:198:41

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P38692

F-NT2RP2003593

PROLINE-RICH PROTEIN MP-2 PRECURSOR.

0.00019:128:32

MUS MUSCULUS (MOUSE).

P05142

F-NT2RP2003599

ATP-DEPENDENT BILE ACID PERMEASE.

0.88:69:34

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32386

F-NT2RP2003655

HYPOTHETICAL 26.3 KD PROTEIN IN OYE2-GND1 INTERGENIC REGION.

2.9e-16:93:47

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P38869

F-NT2RP2003664

HYPOTHETICAL 15.7 KD PROTEIN IN NUP85-SSC1 INTERGENIC REGION.

5.6e-08:121:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P47111

F-NT2RP2003931

ACROSIN PRECURSOR (EC 3.4.21.10).

0.38:20:70

HOMO SAPIENS (HUMAN).

P10323

F-NT2RP2003940

ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).

1.3e-84:126:74

HOMO SAPIENS (HUMAN).

Q03923

5

F-NT2RP2003950

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).

1.5e-05:134:33

HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).

10

P08393

F-NT2RP2004069

HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II.

4.3e-13:68:54

15

CAENORHABDITIS ELEGANS.

Q09297

F-NT2RP2004108

ZINC FINGER PROTEIN 136.

20

8.6e-47:126:67

HOMO SAPIENS (HUMAN).

P52737

F-NT2RP2004141

25

SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).

0.013:127:35

XENOPUS LAEVIS (AFRICAN CLAWED FROG).

P17437

30

F-NT2RP2004179

GLYCEROPHOSPHORYL DIESTER PHOSPHODIESTERASE (EC 3.1.4.46) (GLYCEROPHOSPHODIESTER PHOSPHODIESTERASE).

5.9e-10:110:36

ESCHERICHIA COLI.

35

P10908

F-NT2RP2004205

MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR.

4.6e-10:99:34

40

HOMO SAPIENS (HUMAN).

Q16653

F-NT2RP2004447

PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.

45

0.86:48:37

MUS MUSCULUS (MOUSE).

Q01149

F-NT2RP2004495

50

HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.

0.031:135:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P39981

55

F-NT2RP2004524

HYPOTHETICAL 18.7 KD PROTEIN IN HMS1-ABF2 INTERGENIC REGION.

0.042:96:23

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

Q04767

F-NT2RP2004556

SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).

5 0.0082:87:35

HOMO SAPIENS (HUMAN).

P81489

F-NT2RP2004606

10 METALLOPROTEINASE INHIBITOR 1 PRECURSOR (TIMP-1) (ERYTHROID POTENTIATING ACTIVITY) (EPA) (TISSUE INHIBITOR OF METALLOPROTEINASES) (FIBROBLAST COLLAGENASE INHIBITOR) (COLLAGENASE INHIBITOR).

2.2e-57:163:73

HOMO SAPIENS (HUMAN).

15 P01033

F-NT2RP2004648

BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).

3.2e-25:90:62

20 FELIS SILVESTRIS CATUS (CAT).

O19015

F-NT2RP2004670

CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).

25 6.6e-14:108:34

RATTUS NORVEGICUS (RAT).

Q63450

F-NT2RP2004794

HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.

30 5.7e-11:140:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P40857

35 F-NT2RP2004837

F-NT2RP2004847

ADULT ENHANCER FACTOR 1 (AEF-1).

7.9e-09:81:37

40 DROSOPHILA MELANOGASTER (FRUIT FLY).

P39413

F-NT2RP2005027

GLUCOSE TRANSPORTER TYPE 3, BRAIN.

45 3.6e-64:130:96

HOMO SAPIENS (HUMAN).

P11169

F-NT2RP2005069

CCAAT DISPLACEMENT PROTEIN (CDP) (CDP2) (FRAGMENT).

50 0.22:116:32

RATTUS NORVEGICUS (RAT).

P53565

55 F-NT2RP2005163

ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.

5.3e-06:70:38

ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).

P40602

F-NT2RP2005181

HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG).

4.2e-54:153:69

HOMO SAPIENS (HUMAN).

P30825

F-NT2RP2005247

EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).

2.0e-11:106:35

SORGHUM VULGARE (SORGHUM).

P24152

F-NT2RP2005378

A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.

0.11:97:32

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P32323

F-NT2RP2005391

G-BOX BINDING FACTOR (GBF).

5.1e-10:156:30

DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).

P36417

F-NT2RP2005425

M PROTEIN, SEROTYPE 49 PRECURSOR.

2.1e-05:183:27

STREPTOCOCCUS PYOGENES.

P16947

F-NT2RP2005463

OVOMUCOID (FRAGMENT).

1.0:21:52

BAMBUSICOLA THORACICA (CHINESE BAMBOO-PARTRIDGE).

P52259

F-NT2RP2005514

MOBC PROTEIN.

1.0:26:53

THIOBACILLUS FERROOXIDANS.

P22899

F-NT2RP2005535

ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).

3.8e-92:243:69

HOMO SAPIENS (HUMAN).

Q03923

F-NT2RP2005541

N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).

8.8e-16:78:51

HOMO SAPIENS (HUMAN).

P15586

- 5 F-NT2RP2005597
DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 4 (EC
2.4.1.109).
7.4e-13:99:34
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P46971
- 10 F-NT2RP2005632
ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENY-
LYL CYCLASE).
3.0e-05:73:43
CANIS FAMILIARIS (DOG).
P30803
- 15 F-NT2RP2005666
HEPATOCTE NUCLEAR FACTOR 3-BETA (HNF-3B).
0.086:105:31
MUS MUSCULUS (MOUSE).
P35583
- 20 F-NT2RP2005774
ZINC FINGER PROTEIN 136.
7.8e-33:128:57
HOMO SAPIENS (HUMAN).
P52737
- 25 F-NT2RP2005878
PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).
6.8e-23:96:48
MUS MUSCULUS (MOUSE).
070503
- 30 F-NT2RP2005883
DOPAMINE-BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA- HYDROXYLASE)
(DBH).
6.4e-23:185:32
RATTUS NORVEGICUS (RAT).
Q05754
- 40 F-NT2RP2005887
DNA-DIRECTED RNA POLYMERASE SUBUNIT K (EC 2.7.7.6).
1.0:40:30
METHANOCOCCUS JANNASCHII.
Q57650
- 45 F-NT2RP2005941
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
3.5e-08:136:32
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- 50 F-NT2RP2005994
HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.
4.4e-36:144:47
CAENORHABDITIS ELEGANS.
P49191
- 55 F-NT2RP2006004

EP 1 130 094 A2

- BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40) (DERMATAN SULFATE PROTEOGLYCAN-II) (DSPG).
0.030:28:50
RATTUS NORVEGICUS (RAT).
5 Q01129
- F-NT2RP2006042
HYPOTHETICAL PROTEIN KIAA0144.
1.2e-22:228:39
10 HOMO SAPIENS (HUMAN).
Q14157
- F-NT2RP2006092
TRANSCRIPTIONAL ACTIVATOR FE65.
15 3.1e-27:101:54
RATTUS NORVEGICUS (RAT).
P46933
- F-NT2RP2006099
20 SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
7.0e-07:123:34
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- F-NT2RP2006134
25 TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (EARLY PROTEIN 0) (EP0).
0.0041:118:30
PSEUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).
P29129
30
- F-NT2RP2006269
DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 4 (EC 2.4.1.109).
6.3e-17:119:36
35 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P46971
- F-NT2RP2006512
GNS1 PROTEIN.
8.6e-14:186:30
40 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P25358
- F-NT2RP3000011
PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
45 2.9e-12:137:32
THERMOMONOSPORA CURVATA.
P49695
- F-NT2RP3000022
50 SERINE/THREONINE-PROTEIN KINASE MAK (EC 2.7.1.-) (MALE GERM CELL-ASSOCIATED KINASE).
1.6e-47:121:79
RATTUS NORVEGICUS (RAT).
P20793
- F-NT2RP3000059
55 COLLAGEN ALPHA 1(III) CHAIN.
1.5e-05:211:33
BOS TAURUS (BOVINE).

P04258

F-NT2RP3000063
EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).
4.2e-23:230:28
ZEA MAYS (MAIZE).
P14918

F-NT2RP3000125
CARBOXYPEPTIDASE KEX1 PRECURSOR (EC 3.4.16.6) (CARBOXYPEPTIDASE D).
2.3e-08:110:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P09620

F-NT2RP3000148
ZINC FINGER PROTEIN 133.
1.4e-34:84:48
HOMO SAPIENS (HUMAN).
P52736

F-NT2RP3000169
SMALL PROLINE-RICH PROTEIN 2-1.
0.00092:14:57
HOMO SAPIENS (HUMAN).
P35326

F-NT2RP3000171
24.1 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION.
4.6e-10:134:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P28707

F-NT2RP3000172
CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).
1.8e-33:161:42
RATTUS NORVEGICUS (RAT).
Q63450

F-NT2RP3000201
SERINE/THREONINE-PROTEIN KINASE MIG-15 (EC 2.7.1.-).
4.1e-79:254:64
CAENORHABDITIS ELEGANS.
Q23356

F-NT2RP3000232
ZINC FINGER PROTEIN 184 (FRAGMENT).
8.5e-23:119:45
HOMO SAPIENS (HUMAN).
Q99676

F-NT2RP3000304
LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2-MAC-
ROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER) (CD91).
9.8e-36:172:43
HOMO SAPIENS (HUMAN).
Q07954

F-NT2RP3000378

PAIRED AMPHIPATHIC HELIX PROTEIN.
2.7e-26:186:36
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P22579

5

F-NT2RP3000427
5E5 ANTIGEN.
0.086:204:31
RATTUS NORVEGICUS (RAT).
Q63003

10

F-NT2RP3000436
PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).
1.3e-23:106:33
CAENORHABDITIS ELEGANS.
Q11067

15

F-NT2RP3000444
TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).
0.00052:166:36
HOMO SAPIENS (HUMAN).
000268

20

F-NT2RP3000460
PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.
1.0e-98:194:100
RATTUS NORVEGICUS (RAT).
P38378

25

F-NT2RP3000481
NONSENSE-MEDIATED MRNA DECAY PROTEIN 5.
7.4e-19:217:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P46970

30

F-NT2RP3000616
BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).
1.2e-13:115:33
BOS TAURUS (BOVINE).
P21793

35

F-NT2RP3000645
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
2.3e-10:237:30
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

45

F-NT2RP3000652
ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).
3.1e-106:283:67
HOMO SAPIENS (HUMAN).
Q03923

50

F-NT2RP3000676
ADP/ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP TRANSLOCASE 1) (AD-
ENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).
7.4e-07:102:32
HOMO SAPIENS (HUMAN).

55

- P12235
- F-NT2RP3000677
MHC CLASS II REGULATORY FACTOR RFX1 (RFX) (ENHANCER FACTOR C) (EF-C).
5 1.5e-27:66:54
HOMO SAPIENS (HUMAN).
P22670
- F-NT2RP3000721
10. HYPOTHETICAL 62.5 KD PROTEIN IN SEC53-ACT1 INTERGENIC REGION.
1.6e-22:208:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P43560
- F-NT2RP3000789
15. ONCONEURAL VENTRAL ANTIGEN-1 (NOVA-1) (PARANEOPLASTIC RI ANTIGEN) (VENTRAL NEURON-SPECIFIC PROTEIN 1).
1.0e-07:190:26
HOMO SAPIENS (HUMAN).
20 P51513
- F-NT2RP3000818
HYPOTHETICAL 67.5 KD PROTEIN IN APE1/LAP4-CWP1 INTERGENIC REGION.
5.9e-05:100:32
25. SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P34248
- F-NT2RP3000820
BIOTIN SYNTHASE (EC 2.8.1.6) (BIOTIN SYNTHETASE).
30 0.92:97:26
SYNECHOCYSTIS SP. (STRAIN PCC 6803).
P73538
- F-NT2RP3000838
35. SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
6.4e-07:231:31
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437
- F-NT2RP3000871
40. COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
2.8e-07:221:33
RATTUS NORVEGICUS (RAT).
45 P02454
- F-NT2RP3000907
PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).
2.2e-41:104:48
50. SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39986
- F-NT2RP3000921
BASEMENT MEMBRANE-SPECIFIC HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN PRECURSOR
(HSPG) (PERLECAN) (PLC).
55 4.5e-08:149:31
HOMO SAPIENS (HUMAN).
P98160

- 5 F-NT2RP3001012
HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.
5.5e-06:37:51
PLASMODIUM LOPHURAE.
P04929
- 10 F-NT2RP3001044
RNA POLYMERASE PRINCIPAL SIGMA FACTOR HRDA.
0.10:61:31
STREPTOMYCES COELICOLOR.
P18182
- 15 F-NT2RP3001061
GLYCOPROTEIN X PRECURSOR.
0.00011:140:27
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968
- 20 F-NT2RP3001159
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
1.1e-09:249:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323
- 25 F-NT2RP3001170
POU DOMAIN PROTEIN 1 (DJPOU1).
0.020:173:29
DUGESIA JAPONICA (PLANARIAN).
P31370
- 30 F-NT2RP3001195
GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).
1.2e-14:180:30
ESCHERICHIA COLI.
35 P37021
- 40 F-NT2RP3001240
PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.
3.1e-118:229:88
RATTUS NORVEGICUS (RAT).
P38378
- 45 F-NT2RP3001271
EBNA-1 NUCLEAR PROTEIN.
2.3e-08:113:45
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211
- 50 F-NT2RP3001322
PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38) (ENDOPLASMIC RETICULUM CA²⁺-AT-
PASE).
1.7e-23:222:29
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P39524
- 55 F-NT2RP3001388
SYNAPTOTAGMIN IV.
4.8e-19:168:38

RATTUS NORVEGICUS (RAT).
P50232

5 F-NT2RP3001542
TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).
2.7e-12:132:37
HOMO SAPIENS (HUMAN).
Q13829

10 F-NT2RP3001560
SYNAPSINS IA AND IB.
0.59:104:35
BOS TAURUS (BOVINE).
P17599

15 F-NT2RP3001592
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR.
1.3e-11:75:46
ORYZA SATIVA (RICE).
20 P29834

F-NT2RP3001650
CCAAT DISPLACEMENT PROTEIN (HOMEBOX PROTEIN CLOX) (CLOX-1) (FRAGMENT).
0.23:119:36
25 CANIS FAMILIARIS (DOG).
P39881

F-NT2RP3001685
HYPOTHETICAL PROTEIN IN MMSB 3'REGION (ORF1) (FRAGMENT).
2.2e-48:207:48
30 PSEUDOMONAS AERUGINOSA.
P28812

F-NT2RP3001738
35 CYTOCHROME B5.
9.5e-13:133:33
ORYCTOLAGUS CUNICULUS (RABBIT).
P00169

40 F-NT2RP3001754
SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).
7.9e-05:117:29
HOMO SAPIENS (HUMAN).
P17600

45 F-NT2RP3001858
CUTICLE COLLAGEN 2.
0.030:118:35
CAENORHABDITIS ELEGANS.
50 P17656

F-NT2RP3001976
ZINC FINGER PROTEIN 140.
7.8e-24:122:52
55 HOMO SAPIENS (HUMAN).
P52738

F-NT2RP3002015

- PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
0.018:224:30
GALLUS GALLUS (CHICKEN).
P02457
5. F-NT2RP3002160
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
0.0058:206:29
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
10 P17437
- F-NT2RP3002281
HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).
1.3e-14:86:40
15 HOMO SAPIENS (HUMAN).
P52597
- F-NT2RP3002286
ETS-DOMAIN TRANSCRIPTION FACTOR ERF.
20 0.65:128:29
HOMO SAPIENS (HUMAN).
P50548
- F-NT2RP3002311
25 BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA-GALACTOSIDASE).
6.1e-46:172:54
FELIS SILVESTRIS CATUS (CAT).
O19015
- F-NT2RP3002324
30 HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REGION.
0.012:23:65
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53245
- F-NT2RP3002342
35 HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CAN1 INTERGENIC REGION.
1.8e-13:219:26
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
40 P39981
- F-NT2RP3002353
REGULATORY PROTEIN E2.
0.0027:167:31
45 HUMAN PAPILLOMAVIRUS TYPE 8.
P06422
- F-NT2RP3002409
50 MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEM-
BRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE
OF OUTER MEMBRANE TOM70).
9.9e-09:93:34
NEUROSPORA CRASSA.
P23231
- 55 F-NT2RP3002411
PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).
5.6e-107:254:80

MUS MUSCULUS (MOUSE).
070503

5 F-NT2RP3002448
TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).
1.5e-05:163:33
HOMO SAPIENS (HUMAN).
000268

10 F-NT2RP3002571
HYPOTHETICAL 116.3 KD PROTEIN C26F1.09 IN CHROMOSOME I.
6.4e-23:172:33
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q10496

15 F-NT2RP3002664
CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).
0.062:47:29
HOMO SAPIENS (HUMAN).
20 P18850

F-NT2RP3002721
CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).
6.2e-140:283:92
25 SUS SCROFA (PIG).
P00889

F-NT2RP3002737
VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.9.
30 4.1e-40:136:61
MUS MUSCULUS (MOUSE).
P97414

F-NT2RP3002738
35 SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE S).
0.029:195:28
HOMO SAPIENS (HUMAN).
P10163

40 F-NT2RP3002790
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
1.7e-08:130:36
MUS MUSCULUS (MOUSE).
P05142

45 F-NT2RP3002836
TRANSMEMBRANE PROTEIN SEX PRECURSOR.
8.9e-24:119:43
HOMO SAPIENS (HUMAN).
50 P51805

F-NT2RP3002887
SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAG-
55 MENT).
2.9e-11:198:34
HOMO SAPIENS (HUMAN).
P02812

F-NT2RP3002900
 COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).
 2.8e-18:109:41
 CRICETULUS GRISEUS (CHINESE HAMSTER).
 5 P49020

F-NT2RP3002958
 TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR.
 6.4e-06:172:27
 10 RATTUS NORVEGICUS (RAT).
 P19814

F-NT2RP3002983
 COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
 15 4.4e-05:106:41
 BOS TAURUS (BOVINE).
 P02453

F-NT2RP3003000
 20 SODIUM CHANNEL PROTEIN (NA⁺ CHANNEL).
 9.7e-30:221:31
 ELECTROPHORUS ELECTRICUS (ELECTRIC EEL).
 P02719

F-NT2RP3003076
 25 ENVELOPE GLYCOPROTEIN GP340 (MEMBRANE ANTIGEN) (MA) [CONTAINS: GLYCOPROTEIN GP220].
 0.00033:173:30
 EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
 P03200

F-NT2RP3003354
 30 SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 3.
 2.0e-54:204:51
 MUS MUSCULUS (MOUSE).
 35 035609

F-NT2RP3003448
 PROTEASE DEGS PRECURSOR (EC 3.4.21.-).
 4.0e-05:112:33
 40 ESCHERICHIA COLI.
 P31137

F-NT2RP3003469
 45 !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!
 1.2e-17:70:64
 HOMO SAPIENS (HUMAN).
 P39194

F-NT2RP3003473
 50 BACTENECIN 7 PRECURSOR (BAC7) (PR-59).
 0.0037:33:63
 BOS TAURUS (BOVINE).
 P19661

F-NT2RP3003527
 55 SERINE/THREONINE-SPECIFIC PROTEIN KINASE MINIBRAIN HOMOLOG (EC 2.7.1.-) (HP86) (DYRK).
 1.8e-53:159:69
 HOMO SAPIENS (HUMAN).

- Q13627
- 5 F-NT2RP3003532
OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (FRAGMENT).
2.3e-114:219:97
HOMO SAPIENS (HUMAN).
P41217
- 10 F-NT2RP3003535
HYPOTHETICAL 7.2 KD PROTEIN IN RPS2 3 REGION (ORF57).
0.98:36:30
ASTASIA LONGA (EUGLENOPHYCEAN ALGA).
P34774
- 15 F-NT2RP3003559
MALE SPECIFIC SPERM PROTEIN MST84DB.
0.047:29:48
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q01643
- 20 F-NT2RP3003614
TRYPSIN INHIBITOR II (BDTI-II).
0.98:23:39
BRYONIA DIOICA (RED BRYONY).
P11968
- 25 F-NT2RP3003729
HYPOTHETICAL 42.1 KD PROTEIN IN SNZ1-YPK2 INTERGENIC REGION.
4.1e-11:204:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
Q03151
- 30 F-NT2RP3003849
PROTEIN KINASE C, BRAIN ISOZYME (EC 2.7.1.-) (PKC) (DPKC53E(BR)).
9.7e-17:126:34
DROSOPHILA MELANOGASTER (FRUIT FLY).
P05130
- 35 F-NT2RP3003874
MYOSIN I ALPHA (MMI-ALPHA).
3.1e-64:141:84
MUS MUSCULUS (MOUSE).
P46735
- 40 F-NT2RP3003939
CELL DIVISION PROTEIN FTSH HOMOLOG 4 (EC 3.4.24.-).
7.1e-34:76:61
SYNECHOCYSTIS SP. (STRAIN PCC 6803).
P72991
- 45 F-NT2RP3003963
HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.
0.95:31:38
HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).
Q48251
- 50 F-NT2RP3004000
DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).

7.1e-07:187:29
CRICETULUS GRISEUS (CHINESE HAMSTER).
P11414

5 F-NT2RP3004025
EBNA-1 NUCLEAR PROTEIN.
0.022:79:40
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

10 F-NT2RP3004067
COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.
5.0e-07:184:35
HOMO SAPIENS (HUMAN).
15 Q03692

F-NT2RP3004075
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN PRECURSOR.
2.9e-07:92:40
20 HORDEUM VULGARE (BARLEY).
P17816

F-NT2RP3004083
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).
25 0.013:24:45
COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).
P50682

F-NT2RP3004090
30 SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.
1.2e-07:195:29
DROSOPHILA ERECTA (FRUIT FLY).
P13730

35 F-NT2RP3004119
PEREGRIN (BR140 PROTEIN).
4.1e-40:227:43
HOMO SAPIENS (HUMAN).
P55201

40 F-NT2RP3004130
CELL SURFACE ANTIGEN 114/A10 PRECURSOR.
2.4e-08:71:42
MUS MUSCULUS (MOUSE).
45 P19467

F-NT2RP3004133
GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
1.5e-28:111:44
50 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P43636

F-NT2RP3004202
55 PROLINE-RICH PROTEIN MP-2 PRECURSOR.
3.0e-06:104:37
MUS MUSCULUS (MOUSE).
P05142

- 5 F-NT2RP3004294
HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION.
8.8e-10:129:31
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53288
- 10 F-NT2RP3004309
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
1.9e-05:212:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32323
- 15 F-NT2RP3004321
REGULATORY PROTEIN SIR2 HOMOLOG (LMSIR2RP).
2.8e-09:81:40
LEISHMANIA MAJOR.
Q25337
- 20 F-NT2RP3004345
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 2 PRECURSOR.
1.3e-11:75:46
ORYZA SATIVA (RICE).
P29834
- 25 F-NT2RP3004355
HYDROGENASE EXPRESSION/FORMATION PROTEIN HUPV.
0.81:154:26
AZOTOBACTER CHROOCOCCUM MCD 1.
Q43959
- 30 F-NT2RP3004374
HOMEODOMAIN PROTEIN HOX-A2.
0.28:77:37
GALLUS GALLUS (CHICKEN).
Q08727
- 35 F-NT2RP3004406
HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION.
4.9e-18:165:33
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P40544
- 45 F-NT2RP3004481
BUTYROPHILIN PRECURSOR (BT).
4.0e-13:152:31
HOMO SAPIENS (HUMAN).
Q13410
- 50 F-NT2RP3004552
COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).
3.4e-05:211:28
HOMO SAPIENS (HUMAN).
P17927
- 55 F-NT2RP3004557
INTERFERON GAMMA UP-REGULATED I-5111 PROTEIN PRECURSOR (IGUP I-5111).
1.6e-23:129:35
HOMO SAPIENS (HUMAN).

Q06323

F-NT2RP3004625

GLYCOPROTEIN X PRECURSOR.

5

2.4e-10:225:25

EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).

P28968

F-NT2RP3004640

10

ENAMELIN (TUFTELIN).

2.6e-70:167:85

BOS TAURUS (BOVINE).

P27628

15

F-NT2RP3004647

ADP/ATP CARRIER PROTEIN, HEART/SKELETAL MUSCLE ISOFORM T1 (ADP/ATP TRANSLOCASE 1) (AD-ENINE NUCLEOTIDE TRANSLOCATOR 1) (ANT 1).

4.6e-10:116:34

HOMO SAPIENS (HUMAN).

20

P12235

F-NT2RP4000108

NEUROFILAMENT TRIPLET L PROTEIN (68 KD NEUROFILAMENT PROTEIN) (NF-L) (NF68).

3.4e-107:255:87

25

RATTUS NORVEGICUS (RAT).

P19527

F-NT2RP4000634

MAPK/ERK KINASE KINASE 2 (EC 2.7.1.-) (MEK KINASE 2) (MEKK 2).

30

7.9e-142:267:88

MUS MUSCULUS (MOUSE).

Q61083

F-NT2RP4000962

35

SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).

1.5e-13:158:31

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P08458

40

F-NT2RP4001001

F-NT2RP4001009

POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN- SPECIFIC ENDOPROTEASE 1) (PPSEP 1).

45

7.7e-24:235:31

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

Q10071

F-NT2RP4001467

50

5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN).

1.2e-120:237:97

HOMO SAPIENS (HUMAN).

P21589

55

F-NT2RP4001877

GLYCINE-RICH RNA-BINDING PROTEIN.

1.4e-08:89:34

DAUCUS CAROTA (CARROT).

Q03878

F-NT2RP4001879
VERY HYPOTHETICAL 8.9 KD PROTEIN CY441.05 PRECURSOR.
0.98:49:34
MYCOBACTERIUM TUBERCULOSIS.
P71934

F-NT2RP4002187
PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).
4.5e-98:246:78
MUS MUSCULUS (MOUSE).
070503

F-NT2RP4002451
CUTICLE COLLAGEN 2.
0.85:92:35
CAENORHABDITIS ELEGANS.
P17656

F-NT2RP4002715
HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REGION.
0.47:31:48
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53245

F-NT2RP4002750
HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID
TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RET-
ROVIRUS RECEPTOR HOMOLOG).
3.3e-63:185:67
HOMO SAPIENS (HUMAN).
P30825

F-OVARC1000003
RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANS-
PORTER 2) (NA(+)/PI COTRANSPORTER 2) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 2) (RE-
NAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2).
2.2e-82:197:72
HOMO SAPIENS (HUMAN).
Q06495

F-OVARC1000090
HOMEODOMAIN PROTEIN HOX-B1 (GHOX-LAB).
0.049:120:32
GALLUS GALLUS (CHICKEN).
P31259

F-OVARC1000105
UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN
CARRIER PROTEIN).
8.6e-47:159:58
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P33296

F-OVARC1000137
HYPOTHETICAL 22.7 KD PROTEIN IN PAS1-MST1 INTERGENIC REGION.
0.058:28:64

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P36015

5 F-OVARC1000208
!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!
2.2e-12:51:74
HOMO SAPIENS (HUMAN).
P39195

10 F-OVARC1000255
TYROSINE-PROTEIN KINASE SYK (EC 2.7.1.112) (SPLEEN TYROSINE KINASE).
1.1e-112:144:86
HOMO SAPIENS (HUMAN).
P43405

15 F-OVARC1000275
GASTRIN PRECURSOR.
0.11:59:37
HOMO SAPIENS (HUMAN).
20 P01350

F-OVARC1000298
PROLINE-RICH PROTEIN MP-3 (FRAGMENT).
0.014:74:39
25 MUS MUSCULUS (MOUSE).
P05143

F-OVARC1000307
EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).
30 1.0:33:54
NICOTIANA TABACUM (COMMON TOBACCO).
P13983

F-OVARC1000313
35 PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72) (CALCIUM-BINDING PRO-
TEIN 2) (CABP2).
4.0e-15:127:37
RATTUS NORVEGICUS (RAT).
P38659

40 F-OVARC1000331
GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE).
2.0e-24:64:84
HOMO SAPIENS (HUMAN).
45 P36959

F-OVARC1000410
FIBRINOGEN-LIKE PROTEIN A PRECURSOR (FREPA).
1.9e-44:229:41
50 PARASTICHOPUS PARVIMENSIS (SEA CUCUMBER).
P19477

F-OVARC1000439
55 SALIVARY GLUE PROTEIN SGS-7 PRECURSOR.
0.99:41:43
DROSOPHILA MELANOGASTER (FRUIT FLY).
P02841

- 5 F-OVARC1000467
GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).
0.0061:30:63
LYCOPERSICON ESCULENTUM (TOMATO).
Q01157
- 10 F-OVARC1000529
PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL 101 W (EC 2.7.1.-).
1.5e-20:127:42
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P34244
- 15 F-OVARC1000553
DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (THYMOCYTE-ACTIVATING MOLECULE) (THAM).
7.6e-26:169:40
MUS MUSCULUS (MOUSE).
P28843
- 20 F-OVARC1000775
METALLOTHIONEIN (MT).
0.91:31:38
CARASSIUS AURATUS (GOLDFISH).
P52723
- 25 F-OVARC1000811
COAGULATION FACTOR XII PRECURSOR (EC 3.4.21.38) (HAGEMAN FACTOR) (HAF).
2.8e-11:69:43
HOMO SAPIENS (HUMAN).
P00748
- 30 F-OVARC1000853
CUTICLE COLLAGEN 40.
0.00013:130:33
CAENORHABDITIS ELEGANS.
P34804
- 35 F-OVARC1000873
MALE SPECIFIC SPERM PROTEIN MST84DB.
0.00015:53:33
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q01643
- 45 F-OVARC1000916
GALACTOSYLTRANSFERASE ASSOCIATED PROTEIN KINASE P58/GTA (EC 2.7.1.-).
2.5e-26:109:53
MUS MUSCULUS (MOUSE).
P24788
- 50 F-OVARC1000956
D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
0.00073:115:33
HOMO SAPIENS (HUMAN).
P21917
- 55 F-OVARC1000995
POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L2 (SNF2-ALPHA).
0.00031:139:25
HOMO SAPIENS (HUMAN).

P51531

F-OVARC1001030

5E5 ANTIGEN.

1.9e-09:89:41

RATTUS NORVEGICUS (RAT).

Q63003

F-OVARC1001049

PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.

1.5e-08:146:38

GALLUS GALLUS (CHICKEN).

P02457

F-OVARC1001086

VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LVI); PHOSVITIN (PV); LIPOVITELLIN II (LVII); YGP40].

5.3e-08:182:32

GALLUS GALLUS (CHICKEN).

P02845

F-OVARC1001132

GC-RICH SEQUENCE DNA-BINDING FACTOR (GCF) (TRANSCRIPTION FACTOR 9) (TCF-9).

9.2e-40:229:37

HOMO SAPIENS (HUMAN).

P16383

F-OVARC1001163

HYPOTHETICAL 49.3 KD PROTEIN C30D 11.06C IN CHROMOSOME I.

8.8e-05:38:44

SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).

Q09906

F-OVARC1001222

AMELOGENIN, CLASS I PRECURSOR.

0.72:96:31

BOS TAURUS (BOVINE).

P02817

F-OVARC1001260

F-OVARC1001336

RENAL SODIUM-DEPENDENT PHOSPHATE TRANSPORT PROTEIN 2 (SODIUM/PHOSPHATE COTRANSPORTER 2) (NA(+)/PI COTRANSPORTER 2) (RENAL SODIUM-PHOSPHATE TRANSPORT PROTEIN 2) (RENAL NA+-DEPENDENT PHOSPHATE COTRANSPORTER 2).

1.1e-33:103:71

RATTUS NORVEGICUS (RAT).

Q06496

F-OVARC1001338

SERINE/THREONINE-PROTEIN KINASE UNC-51 (EC 2.7.1.-).

3.8e-30:89:46

CAENORHABDITIS ELEGANS.

Q23023

F-OVARC1001569

ACROSIN PRECURSOR (EC 3.4.21.10) (53 KD FUCOSE-BINDING PROTEIN).

2.2e-06:28:64

SUS SCROFA (PIG).
P08001

5 F-OVARC1001570
CATHEPSIN E PRECURSOR (EC 3.4.23.34).
1.8e-09:121:33
CAVIA PORCELLUS (GUINEA PIG).
P25796

10 F-OVARC1001596
REGULATORY PROTEIN E2.
0.33:77:37
HUMAN PAPILLOMAVIRUS TYPE 14.
P36783

15 F-OVARC1001607
ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC
2.4.1.143) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANS-
20 FERASE II) (BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE II) (GNT-II) (GLCNAC-T II).
1.0e-28:69:84
HOMO SAPIENS (HUMAN).
Q10469

25 F-OVARC1001725

F-OVARC1001727

F-OVARC1001807
EARLY RESPONSE PROTEIN NAK1 (TR3 ORPHAN RECEPTOR).
30 2.4e-51:153:75
HOMO SAPIENS (HUMAN).
P22736

35 F-OVARC1001833
CIS-GOLGI MATRIX PROTEIN GM130.
1.2e-55:169:75
RATTUS NORVEGICUS (RAT).
Q62839

40 F-OVARC1001952
EBNA-1 NUCLEAR PROTEIN.
3.5e-19:130:43
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

45 F-OVARC1001991
HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT).
3.7e-16:141:43
HOMO SAPIENS (HUMAN).
50 Q14681

F-OVARC1002058
LAMININ ALPHA-5 CHAIN (FRAGMENT).
2.8e-22:163:33
55 MUS MUSCULUS (MOUSE).
Q61001

F-OVARC1002178

EP 1 130 094 A2

TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE110) (VMW110) (ALPHA-0 PROTEIN).

0.12:73:36

HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).

P08393

F-PLACE1000033

VON WILLEBRAND FACTOR PRECURSOR.

1.7e-19:190:28

CANIS FAMILIARIS (DOG).

Q28295

F-PLACE1000231

DNA-BINDING PROTEIN MNB1A.

0.24:60:33

ZEA MAYS (MAIZE).

P38564

F-PLACE1000258

ZINC FINGER PROTEIN 177.

3.6e-19:55:61

HOMO SAPIENS (HUMAN).

Q13360

F-PLACE1000442

ZINC FINGER PROTEIN 136.

1.7e-80:180:72

HOMO SAPIENS (HUMAN).

P52737

F-PLACE1000560

COLICIN E9 (EC 3.1.21.1).

0.015:47:44

ESCHERICHIA COLI.

P09883

F-PLACE1000740

NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3).

1.6e-05:75:36

MUS MUSCULUS (MOUSE).

P31695

F-PLACE1000907

ZINC FINGER PROTEIN 141.

2.8e-15:43:88

HOMO SAPIENS (HUMAN).

Q15928

F-PLACE1000912

PROBABLE E4 PROTEIN (E1^E4).

0.19:46:36

HUMAN PAPILLOMAVIRUS TYPE 6B.

P06459

F-PLACE1000914

MALE SPECIFIC SPERM PROTEIN MST87F.

0.054:27:44

DROSOPHILA MELANOGASTER (FRUIT FLY).

- P08175
- F-PLACE1000927
HYPOTHETICAL PROTEIN HI0044.
5 3.9e-07:139:30
HAEMOPHILUS INFLUENZAE.
P44477
- F-PLACE1000986
- 10 F-PLACE1001016
SODIUM CHANNEL PROTEIN, BRAIN II ALPHA SUBUNIT.
2.7e-05:120:32
RATTUS NORVEGICUS (RAT).
15 P04775
- F-PLACE1001100
- F-PLACE1001114
20 PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.
2.5e-07:250:28
MUS MUSCULUS (MOUSE).
P11087
- 25 F-PLACE1001123
INTESTINAL MEMBRANE A4 PROTEIN (DIFFERENTIATION-DEPENDENT PROTEIN A4).
6.2e-09:95:31
HOMO SAPIENS (HUMAN).
Q04941
- 30 F-PLACE1001183
NONHISTONE CHROMOSOMAL PROTEIN HMG-17.
0.31:52:34
GALLUS GALLUS (CHICKEN).
35 P02314
- F-PLACE1001229
NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).
1.0:38:47
40 ARTEMIA SAUNA (BRINE SHRIMP).
P19047
- F-PLACE1001231
SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSPORTER).
45 4.7e-06:181:27
ORYCTOLAGUS CUNICULUS (RABBIT).
P11170
- 50 F-PLACE1001340
MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).
6.5e-14:136:29
55 NEUROSPORA CRASSA.
P23231
- F-PLACE1001401

- HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGE FC RECEPTOR, BETA-SUBUNIT).
1.3e-11:103:40
RATTUS NORVEGICUS (RAT).
5 P13386
- F-PLACE1001407
INTEGUMENTARY MUCIN C.1 (FIM-C.1) (FRAGMENT).
0.013:121:32
10 XENOPUS LAEVIS (AFRICAN CLAWED FROG).
Q05049
- F-PLACE1001464
5'-NUCLEOTIDASE PRECURSOR (EC 3.1.3.5) (ECTO-NUCLEOTIDASE) (5'-NT) (CD73 ANTIGEN).
15 1.4e-119:246:89
HOMO SAPIENS (HUMAN).
P21589
- F-PLACE1001500
20 BLOOM'S SYNDROME PROTEIN.
8.3e-26:203:34
HOMO SAPIENS (HUMAN).
P54132
- F-PLACE1001516
25 GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-
GLUCAN GLUCOHYDROLASE).
7.4e-07:204:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
30 P08640
- F-PLACE1001536
- F-PLACE1001564
35 LEUCOCYTE ANTIGEN CD97 PRECURSOR.
2.1e-09:170:24
HOMO SAPIENS (HUMAN).
P48960
- F-PLACE1001655
40 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV2.1 (DRK1).
4.0e-34:189:39
RATTUS NORVEGICUS (RAT).
P15387
- F-PLACE1001788
45 HYPOTHETICAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME I.
6.2e-21:75:58
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
50 Q09695
- F-PLACE1001795
HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-SMC3 INTERGENIC REGION PRECURSOR.
3.8e-21:159:40
55 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P47032
- F-PLACE1001836

- ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEMBRANE PROTEIN GP70;
TRANSMEMBRANE PROTEIN P20E].
4.5e-29:134:47
BABOON ENDOGENOUS VIRUS (STRAIN M7).
5 P10269
- F-PLACE1001918
ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-
FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).
10 1.5e-30:228:32
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P32802
- F-PLACE1001949
15 PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).
5.1e-36:210:46
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
Q12697
- F-PLACE1002080
20 HYPOTHETICAL PROTEIN KIAA0288 (HA6116).
3.5e-26:207:45
HOMO SAPIENS (HUMAN).
P56524
- F-PLACE1002095
25 N-ACETYLLACTOSAMINE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1→4)GALACTOSYL-
TRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANS-
FERASE) (GT).
30 0.32:50:34
MUS MUSCULUS (MOUSE).
P15535
- F-PLACE1002153
35 CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (SLAYER PROTEIN 1).
0.00021:214:26
CLOSTRIDIUM THERMOCELLUM.
Q06852
- F-PLACE1002329
40 EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.
1.1e-35:179:44
MUS MUSCULUS (MOUSE).
Q08509
- F-PLACE1002355
45 COMPLEMENT C4 PRECURSOR [CONTAINS: C4A ANAPHYLATOXIN] (FRAGMENTS).
1.0e-14:183:32
BOS TAURUS (BOVINE).
50 P01030
- F-PLACE1002374
CATHEPSIN L PRECURSOR (EC 3.4.22.15) (MAJOR EXCRETED PROTEIN) (MEP).
9.2e-107:225:86
55 HOMO SAPIENS (HUMAN).
P07711
- F-PLACE1002518

HYPOTHETICAL 13.2 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION.

6.1e-05:59:44

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

P38239

5

F-PLACE1002547

MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).

10

1.0e-22:230:31

NEUROSPORA CRASSA.

P23231

F-PLACE1002726

15

COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).

0.61:25:48

ORYCTOLAGUS CUNICULUS (RABBIT).

P02456

F-PLACE1002905

20

ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).

5.0e-31:93:64

BOS TAURUS (BOVINE).

25

P07106

F-PLACE1002911

T-CELL SURFACE PROTEIN TACTILE PRECURSOR (CD96 ANTIGEN).

6.6e-06:95:35

30

HOMO SAPIENS (HUMAN).

P40200

F-PLACE1002967

35

HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCER1) (IGE FC RECEPTOR, BETA-SUBUNIT).

9.4e-08:95:37

MUS MUSCULUS (MOUSE).

P20490

F-PLACE1003135

40

SERINE/THREONINE-PROTEIN KINASE STE20 (EC 2.7.1.-).

1.9e-33:99:50

SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).

Q03497

45

F-PLACE1003163

ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).

9.8e-15:105:38

50

BOS TAURUS (BOVINE).

P07106

F-PLACE1003407

55

CLN5 PROTEIN.

4.2e-109:217:89

HOMO SAPIENS (HUMAN).

075503

- 5 F-PLACE1003428
BIOTINIDASE PRECURSOR (EC 3.5.1.12).
1.0e-36:104:46
HOMO SAPIENS (HUMAN).
P43251
- 10 F-PLACE1003438
HYPOTHETICAL 104.4 KD PROTEIN C17A5.16 IN CHROMOSOME I.
1.1e-10:148:33
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
013776
- 15 F-PLACE1003460
2-HYDROXY-6-KETONONA-2,4-DIENEDIOIC ACID HYDROLASE (EC 3.7.1.-).
0.00028:134:27
ESCHERICHIA COLI.
P77044
- 20 F-PLACE1003529
TRANSCRIPTION REGULATORY PROTEIN SNF5 (SWI/SNF COMPLEX COMPONENT SNF5) (TRANSCRIPTION FACTOR TFE4).
0.00047:157:27
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P18480
- 25 F-PLACE1003573
T-CELL SURFACE GLYCOPROTEIN YE1/48 (T LYMPHOCYTE ANTIGEN A1) (LY49-A ANTIGEN).
0.022:129:25
MUS MUSCULUS (MOUSE).
30 P20937
- 35 F-PLACE1003598
TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).
0.0017:102:44
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).
P29128
- 40 F-PLACE1003644
PROTEIN Q300.
6.7e-05:24:70
MUS MUSCULUS (MOUSE).
Q02722
- 45 F-PLACE1003737
TOLL PROTEIN PRECURSOR.
7.3e-08:203:27
DROSOPHILA MELANOGASTER (FRUIT FLY).
P08953
- 50 F-PLACE1003772
SALIVARY PROLINE-RICH PROTEIN II-1 (FRAGMENT).
3.7e-07:141:32
HOMO SAPIENS (HUMAN).
P81489
- 55 F-PLACE1003839
PROLINE-RICH PROTEIN MP-3 (FRAGMENT).
1.3e-09:201:31

MUS MUSCULUS (MOUSE).
P05143

5 F-PLACE1003845
PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPI-
MERASE).
5.0e-13:103:33
METHANOCOCCUS JANNASCHII.
Q57664

10 F-PLACE1003852
CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1 HORMONE RECEPTOR).
2.0e-18:189:29
HOMO SAPIENS (HUMAN).
15 Q14246

F-PLACE1004028
HYPOTHETICAL 9.7 KD PROTEIN IN PURC-PURL INTERGENIC REGION.
0.97:47:31
20 BACILLUS SUBTILIS.
P12049

F-PLACE1004078
ADSEVERIN (SCINDERIN) (SC).
25 5.3e-98:176:90
BOS TAURUS (BOVINE).
Q28046

F-PLACE1004166
30 CREB-BINDING PROTEIN.
9.6e-08:107:34
HOMO SAPIENS (HUMAN).
Q92793

35 F-PLACE1004168
GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 1.
6.8e-05:147:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P25655

40 F-PLACE1004199
!!!! ALU SUBFAMILY J WARNING ENTRY !!!!
4.2e-05:65:52
HOMO SAPIENS (HUMAN).
45 P39188

F-PLACE1004279
HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.
3.6e-11:166:30
50 CAENORHABDITIS ELEGANS.
P30638

F-PLACE1004282
HISTONE H1C (CLONE XLHW2).
55 0.74:73:26
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P15866

- 5 F-PLACE1004305
RAS-RELATED PROTEIN RAC1.
2.3e-23:161:39
DROSOPHILA MELANOGASTER (FRUIT FLY).
P40792
- 10 F-PLACE1004441
PROBABLE G PROTEIN-COUPLED RECEPTOR GPR1.
5.4e-70:156:89
HOMO SAPIENS (HUMAN).
P46091
- 15 F-PLACE1004450
AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE).
3.1e-40:196:44
RATTUS NORVEGICUS (RAT).
P15684
- 20 F-PLACE1004482
ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).
0.23:26:30
GALLUS GALLUS (CHICKEN).
P14093
- 25 F-PLACE1004492
COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).
1.2e-05:150:34
BOS TAURUS (BOVINE).
P02453
- 30 F-PLACE1004519
ENL PROTEIN.
0.68:170:30
HOMO SAPIENS (HUMAN).
Q03111
- 35 F-PLACE1004520
PREGNANCY-SPECIFIC BETA-1 GLYCOPROTEIN PRECURSOR.
3.5e-50:150:74
HOMO SAPIENS (HUMAN).
P11462
- 40 F-PLACE1004630
INTEGRIN BETA-6 SUBUNIT PRECURSOR.
9.1e-31:189:39
HOMO SAPIENS (HUMAN).
P18564
- 45 F-PLACE1004637
MALE SPECIFIC SPERM PROTEIN MST84DA.
0.47:29:44
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q01642
- 50 F-PLACE1004648
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
8.4e-05:89:40
MUS MUSCULUS (MOUSE).

- P05142
- F-PLACE1004816
MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.
5 1.0e-25:117:46
HOMO SAPIENS (HUMAN).
P55083
- F-PLACE1004887
10 SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.
8.4e-09:195:30
DROSOPHILA ERECTA (FRUIT FLY).
P13730
- F-PLACE1005003
15 PROSTASIN PRECURSOR (EC 3.4.21.-).
1.2e-24:139:40
HOMO SAPIENS (HUMAN).
Q16651
- F-PLACE1005005
20 UBIQUITIN-CONJUGATING ENZYME E2 G2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).
2.5e-28:51:84
25 HOMO SAPIENS (HUMAN).
P56554
- F-PLACE1005031
30 CHLORINE CHANNEL PROTEIN P64.
2.7e-52:142:76
BOS TAURUS (BOVINE).
P35526
- F-PLACE1005239
35 SPLICING FACTOR, ARGININE/SERINE-RICH 6 (PRE-MRNA SPLICING FACTOR SRP55) (FRAGMENT).
0.27:78:26
ORYCTOLAGUS CUNICULUS (RABBIT).
018776
- F-PLACE1005250
40 HYPOTHETICAL 9.0 KD PROTEIN IN ADH4 5'REGION.
0.22:35:48
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53056
- F-PLACE1005383
45 FIBRILLIN 1 PRECURSOR.
6.7e-09:134:32
MUS MUSCULUS (MOUSE).
50 Q61554
- F-PLACE1005410
PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.
9.5e-105:204:100
55 RATTUS NORVEGICUS (RAT).
P38378
- F-PLACE1005426

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- 5 PREGNANCY-SPECIFIC BETA-1-GLYCOPROTEIN 4 PRECURSOR (PSBG-4).
3.2e-33:184:46
HOMO SAPIENS (HUMAN).
Q00888
- 10 F-PLACE1005519
SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-) (N-RICH KINASE 1).
1.2e-23:143:41
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38692
- 15 F-PLACE1005539
ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) (FRAGMENT).
5.5e-05:94:37
BRASSICA NAPUS (RAPE).
P40603
- 20 F-PLACE1005544
CELL SURFACE A33 ANTIGEN PRECURSOR.
0.00015:132:31
HOMO SAPIENS (HUMAN).
Q99795
- 25 F-PLACE1005569
PROTEOGLYCAN LINK PROTEIN PRECURSOR (CARTILAGE LINK PROTEIN) (LP).
0.00092:122:31
EQUUS CABALLUS (HORSE).
Q28381
- 30 F-PLACE1005601
TOXIN S4C8.
0.34:32:37
DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S MAMBA).
P25683
- 35 F-PLACE1005660
SALIVARY GLUE PROTEIN SGS-7 PRECURSOR.
0.99:41:43
DROSOPHILA MELANOGASTER (FRUIT FLY).
P02841
- 40 F-PLACE1005669
COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN).
0.0078:105:37
HOMO SAPIENS (HUMAN).
Q02388
- 45 F-PLACE1005682
THYROID RECEPTOR INTERACTING PROTEIN 9 (TRIP9).
2.7e-12:81:41
HOMO SAPIENS (HUMAN).
Q15653
- 50 F-PLACE1005725
HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.
7.5e-08:142:31
CAENORHABDITIS ELEGANS.
Q11073

- 5 F-PLACE1005736
RAC-FAMILY SERINE/THREONINE KINASE HOMOLOG (EC 2.7.1.-).
9.0e-11:91:37
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P54644
- 10 F-PLACE1005745
ORM1 PROTEIN.
2.2e-18:137:35
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53224
- 15 F-PLACE1005768
NEUROTOXINS I AND I'PRECURSOR (AAH I AND AAH I').
0.63:13:69
ANDROCTONUS AUSTRALIS HECTOR (SAHARA SCORPION). P01479
- 20 F-PLACE1005815
COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN).
1.8e-12:73:50
HOMO SAPIENS (HUMAN).
P23508
- 25 F-PLACE1005878
CHLORINE CHANNEL PROTEIN P64.
1.6e-49:115:79
BOS TAURUS (BOVINE).
P35526
- 30 F-PLACE1005927
HYPOTHETICAL 35.8 KD PROTEIN C12G12.12 IN CHROMOSOME I.
3.2e-16:152:34
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09875
- 35 F-PLACE1006071
LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN).
4.1e-08:215:26
MUS MUSCULUS (MOUSE).
40 P02469
- 45 F-PLACE1006073
SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).
2.1e-05:137:34
NEPHILA CLAVIPES (ORB SPIDER).
P46804
- 50 F-PLACE1006079
HOMEBOX PROTEIN DLX-3.
1.5e-58:144:83
HOMO SAPIENS (HUMAN).
060479
- 55 F-PLACE1006093
SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).
3.8e-05:72:40
HOMO SAPIENS (HUMAN).
P17600

- 5 F-PLACE1006208
EBNA-2 NUCLEAR PROTEIN.
3.8e-15:28:75
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4). P12978
- 10 F-PLACE1006219
UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)
(FRAGMENT)
2.0e-09:38:42
KLEBSIELLA PNEUMONIAE.
P45602
- 15 F-PLACE1006277
CELL SURFACE A33 ANTIGEN PRECURSOR.
1.2e-07:183:29
HOMO SAPIENS (HUMAN).
Q99795
- 20 F-PLACE1006290
GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
8.2e-39:171:43
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P43636
- 25 F-PLACE1006443
HYPOTHETICAL 60.0 KD PROTEIN IN IMP1-HLJ1 INTERGENIC REGION.
0.0010:155:27
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
Q03795
- 30 F-PLACE1006515
ZINC FINGER Y-CHROMOSOMAL PROTEIN 1.
0.046:98:28
MUS MUSCULUS (MOUSE).
P10925
- 35 F-PLACE1006716
30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADIPOCYTE SPECIFIC
PROTEIN ADIPOQ).
3.6e-25:177:35
MUS MUSCULUS (MOUSE).
Q60994
- 40 F-PLACE1006786
PROBABLE NONSPECIFIC LIPID-TRANSFER PROTEIN (LTP) (BASIC PROTEIN) (WBP) (FRAGMENT).
1.0:19:42
TRITICUM AESTIVUM (WHEAT).
P26913
- 45 F-PLACE1006809
SLS1 PROTEIN PRECURSOR.
0.0011:37:51
YARROWIA LIPOLYTICA (CANDIDA LIPOLYTICA).
Q99158
- 50 F-PLACE1006959
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
5.3e-05:96:41

MUS MUSCULUS (MOUSE).
P05142

5 F-PLACE1007028
EBNA-1 NUCLEAR PROTEIN.
5.9e-09:219:33
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211

10 F-PLACE1007040
SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAG-
MENT).
0.68:138:24
HOMO SAPIENS (HUMAN).
15 P02812

F-PLACE1007077
SERINE/THREONINE-PROTEIN KINASE CLA4 (EC 2.7.1.-).
0.73:177:25
20 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P48562

F-PLACE1007081
COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR).
25 3.0e-20:182:39
BOS TAURUS (BOVINE).
Q28107

F-PLACE1007096
30 HYPOTHETICAL SYMPORTER SLL1374.
2.8e-14:162:30
SYNECHOCYSTIS SP. (STRAIN PCC 6803).
P74168

35 F-PLACE1007296
ER LUMEN PROTEIN RETAINING RECEPTOR 1 (KDEL RECEPTOR 1).
9.4e-50:120:86
HOMO SAPIENS (HUMAN).
P24390

40 F-PLACE1007591
MEIOTIC RECOMBINATION PROTEIN REC104.
0.68:73:31
45 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P33323

F-PLACE1007626
PTB-ASSOCIATED SPLICING FACTOR (PSF).
0.00083:97:34
50 HOMO SAPIENS (HUMAN).
P23246

F-PLACE1007702
55 ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR.
1.9e-08:87:36
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
P40602

- 5 F-PLACE1007845
GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).
1.3e-16:158:40
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P43636
- 10 F-PLACE1007881
HYPOTHETICAL 69.4 KD PROTEIN F13H10.3 IN CHROMOSOME IV.
1.2e-11:113:37
CAENORHABDITIS ELEGANS.
Q19425
- 15 F-PLACE1007971
METALLOTHIONEIN 20-III ISOFORMS A AND B (MT-20-III A AND MT-20-III B).
1.0:32:43
MYTILUS EDULIS (BLUE MUSSEL).
P80253
- 20 F-PLACE1008282
HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-) (HRI).
8.1e-87:178:87
ORYCTOLAGUS CUNICULUS (RABBIT).
P33279
- 25 F-PLACE1008297
MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B).
3.6e-17:187:33
DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).
P90648
- 30 F-PLACE1008359
BEM46 PROTEIN (FRAGMENT).
4.9e-07:103:33
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
P54069
- 35 F-PLACE1008469
D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR).
0.0018:78:37
HOMO SAPIENS (HUMAN).
P21917
- 40 F-PLACE1008549
FLI-1 ONCOGENE (ERGB TRANSCRIPTION FACTOR).
0.0034:89:30
HOMO SAPIENS (HUMAN).
Q01543
- 45 F-PLACE1008657
ADSEVERIN (SCINDERIN) (SC).
6.7e-127:257:91
BOS TAURUS (BOVINE).
Q28046
- 50 F-PLACE1008716
ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.143) (N-GLYCOSYL-OLIGOSACCHARIDE-GLYCOPROTEIN N-ACETYLGLUCOSAMINYLTRANSFERASE II) (BETA-1,2-N-ACETYLGLUCOSAMINYLTRANSFERASE II) (GNT-II) (GLCNAC-T II).

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- 4.5e-20:66:78
HOMO SAPIENS (HUMAN).
Q10469
- 5 F-PLACE1008744
C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN) (PRP).
3.6e-19:221:33
HOMO SAPIENS (HUMAN).
P04003
- 10 F-PLACE1008984
BIOTIN CARBOXYL CARRIER PROTEIN OF ACETYL-COA CARBOXYLASE PRECURSOR (EC 6.4.1.2) (BC-CP).
0.089:61:31
15 GLYCINE MAX (SOYBEAN).
Q42783
- F-PLACE1008985
SYNAPTOTAGMIN V.
20 8.6e-09:123:35
HOMO SAPIENS (HUMAN).
000445
- F-PLACE1009067
25 HYPOTHETICAL 33.4 KD PROTEIN.
4.3e-09:60:50
HOMO SAPIENS (HUMAN).
Q04323
- 30 F-PLACE1009196
SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).
0.050:23:34
GORILLA GORILLA GORILLA (LOWLAND GORILLA).
P35303
- 35 F-PLACE1009279
8.6 KD TRANSGLUTAMINASE SUBSTRATE.
1.4e-07:62:35
TACHYPLEUS TRIDENTATUS (JAPANESE HORSESHOE CRAB).
40 P81281
- F-PLACE1009527
MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).
0.037:71:38
45 HOMO SAPIENS (HUMAN).
Q02817
- F-PLACE1009546
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
50 5.9e-07:86:39
MUS MUSCULUS (MOUSE).
P05142
- F-PLACE1009600
55 TETRACYCLINE RESISTANCE PROTEIN, CLASS H (TETA(H)).
1.7e-08:113:31
PASTEURELLA MULTOCIDA.
P51564

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- 5 F-PLACE1009735
TARNS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (IMMEDIATE-EARLY PROTEIN IE1 10) (VMW110) (AL-
PHA-0 PROTEIN).
2.6e-09:182:35
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P08393
- 10 F-PLACE1009982
REGULATORY PROTEIN E2.
0.99:94:28
HUMAN PAPILLOMAVIRUS TYPE 8.
P06422
- 15 F-PLACE1010011
DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE (EC 2.7.8.2) (SN-1,2-DIACYLGLYCEROL
CHOLINEPHOSPHOTRANSFERASE) (CHOPT).
2.8e-20:119:42
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P17898
- 20 F-PLACE1010078
ORM1 PROTEIN.
3.4e-20:137:37
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53224
- 25 F-PLACE1010081
SERINE/THREONINE-PROTEIN KINASE CTR1 (EC 2.7.1.37).
1.5e-11:147:32
ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).
Q05609
- 30 F-PLACE1010251
NEL-LIKE PROTEIN (FRAGMENT).
1.8e-10:73:42
HOMO SAPIENS (HUMAN).
Q92832
- 40 F-PLACE1010445
HYPOTHETICAL BHLF1 PROTEIN.
0.0042:227:33
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03181
- 45 F-PLACE1010713
PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).
1.5e-77:177:80
MUS MUSCULUS (MOUSE).
070503
- 50 F-PLACE1010784
P2Y PURINOCEPTOR 5 (P2Y5) (PURINERGIC RECEPTOR 5) (6H1).
1.7e-18:102:40
GALLUS GALLUS (CHICKEN).
P32250
- 55 F-PLACE1010827
COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).

- 2.8e-18:109:41
CRICETULUS GRISEUS (CHINESE HAMSTER).
P49020
- 5 F-PLACE1010968
PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATE
PHOSPHOHYDROLASE).
2.3e-06:191:28
DROSOPHILA MELANOGASTER (FRUIT FLY).
10 P16621
- F-PLACE1011045
HYPOTHETICAL 71.4 KD PROTEIN IN NMD3-ENO2 INTERGENIC REGION.
6.0e-14:153:34
15 SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P38862
- F-PLACE1011116
GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-
20 GLUCAN GLUCOHYDROLASE).
2.3e-06:195:27
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08640
- 25 F-PLACE1011181
MSP1 PROTEIN HOMOLOG.
4.3e-06:93:25
CAENORHABDITIS ELEGANS.
P54815
- 30 F-PLACE1011236
HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.
4.1e-17:180:28
CAENORHABDITIS ELEGANS.
35 P30638
- F-PLACE1011364
HYPOTHETICAL 141.2 KD PROTEIN EEED8.9 IN CHROMOSOME II.
2.1e-24:158:41
40 CAENORHABDITIS ELEGANS.
Q09298
- F-PLACE1011407
ZINC FINGER PROTEIN 140.
45 3.8e-10:47:74
HOMO SAPIENS (HUMAN).
P52738
- F-PLACE1011516
50 HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.
1.6e-13:117:34
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53073
- 55 F-PLACE1011708
DORSAL-VENTRAL PATTERNING TOLLOID PROTEIN PRECURSOR (EC 3.4.24.-).
9.9e-22:203:32
DROSOPHILA MELANOGASTER (FRUIT FLY).

P25723

F-PLACE1011824

SERINE/THREONINE-PROTEIN KINASE PAK-BETA (EC 2.7.1.-) (BETA-PAK) (P21-ACTIVATED KINASE 3) (CDC42/RAC EFFECTOR KINASE PAK-B).

1.6e-15:103:36

MUS MUSCULUS (MOUSE).

Q61036

F-PLACE1011978

ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).

3.3e-55:188:50

HOMO SAPIENS (HUMAN).

Q03923

F-PLACE2000118

EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).

2.8e-23:169:43

NICOTIANA TABACUM (COMMON TOBACCO).

P13983

F-PLACE2000219

MALE SPECIFIC SPERM PROTEIN MST84DA.

0.11:29:41

DROSOPHILA MELANOGASTER (FRUIT FLY).

Q01642

F-PLACE3000181

CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).

9.5e-26:193:37

DROSOPHILA MELANOGASTER (FRUIT FLY).

P33450

F-PLACE3000213

COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).

2.3e-23:191:34

HOMO SAPIENS (HUMAN).

P17927

F-PLACE4000354

E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).

3.2e-25:150:30

ORYCTOLAGUS CUNICULUS (RABBIT).

P27113

F-PLACE4000455

IG KAPPA CHAIN PRECURSOR V-III REGION (VG) (FRAGMENT).

0.66:52:36

HOMO SAPIENS (HUMAN).

P04433

F-SKNMC1000004

OPTOMOTOR-BLIND PROTEIN (LETHAL(1)OPTOMOTOR-BLIND) (L(1)OMB) (BIFID PROTEIN).

0.079:88:30

DROSOPHILA MELANOGASTER (FRUIT FLY).

Q24432

- 5 F-SKNMC1000014
SCO-SPONDIN (FRAGMENT).
0.63:60:36
BOS TAURUS (BOVINE).
P98167
- 10 F-SKNMC1000082
PUTATIVE MITOCHONDRIAL CARRIER YGR096W.
2.4e-10:93:34
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53257
- 15 F-THYRO1000036
PROLINE-RICH PROTEIN MP-3 (FRAGMENT).
0.72:69:36
MUS MUSCULUS (MOUSE).
P05143
- 20 F-THYRO1000061
COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).
0.0068:70:38
BOS TAURUS (BOVINE).
P25508
- 25 F-THYRO1000099
SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).
0.0063:207:28
NEPHILA CLAVIPES (ORB SPIDER).
P46804
- 30 F-THYRO1000196
RETINAL-CADHERIN PRECURSOR (R-CADHERIN) (R-CAD).
1.6e-10:134:32
GALLUS GALLUS (CHICKEN).
35 P24503
- 40 F-THYRO1000400
ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN (STOMATIN) (PROTEIN 7.2B).
3.9e-28:163:38
MUS MUSCULUS (MOUSE).
P54116
- 45 F-THYRO1000580
RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17).
3.3e-15:64:62
MUS MUSCULUS (MOUSE).
Q61751
- 50 F-THYRO1000584
EPIDIDYMIS-SPECIFIC ALPHA-MANNOSIDASE (EC 3.2.1.24) (ALPHA-D-MANNOSIDE MANNOHYDROLASE)
(135 KD PROTEIN).
1.5e-89:197:72
SUS SCROFA (PIG).
Q28949
- 55 F-THYRO1000678
GAP JUNCTION BETA-6 PROTEIN (CONNEXIN 30) (CX30).
7.7e-39:89:87

- MUS MUSCULUS (MOUSE).
P70689
- 5 F-THYRO1000776
HIGH AFFINITY SULPHATE TRANSPORTER 2.
3.0e-25:83:50
STYLOSANTHES HAMATA.
P53392
- 10 F-THYRO1000795
MITOCHONDRIAL 2-OXOGLUTARATE/MALATE CARRIER PROTEIN (OGCP).
1.2e-33:227:37
BOS TAURUS (BOVINE).
P22292
- 15 F-THYRO1000846
CUTICLE COLLAGEN 12 PRECURSOR.
6.7e-09:190:33
CAENORHABDITIS ELEGANS.
20 P20630
- F-THYRO1000866
HYPOTHETICAL 146.8 KD PROTEIN C34E10.5 IN CHROMOSOME III.
0.12:85:31
25 CAENORHABDITIS ELEGANS.
P46580
- F-THYRO1000956
PROBABLE G PROTEIN-COUPLE1) RECEPTOR APJ.
30 1.3e-68:165:84
HOMO SAPIENS (HUMAN).
P35414
- F-THYRO1000964
35 TARNS-ACTING TRANSCRIPTIONAL PROTEIN ICP0 (P135 PROTEIN) (IER 2.9/ER2.6).
0.015:170:34
BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).
P29128
- 40 F-THYRO1000999
CRYPTIDIN-RELATED PROTEIN 4C-2 PRECURSOR (CRS4C).
0.28:40:45
MUS MUSCULUS (MOUSE).
45 P50715
- F-THYRO1001063
SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEP-
TIDE IB-6; PEPTIDE P-H].
3.5e-05:232:32
50 HOMO SAPIENS (HUMAN).
P04280
- F-THYRO1001071
SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).
55 0.00061:131:33
XENOPUS LAEVIS (AFRICAN CLAWED FROG).
P17437

- 5 F-THYRO1001102
TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).
0.25:94:38
HOMO SAPIENS (HUMAN).
000268
- 10 F-THYRO1001113
SYNAPTOTAGMIN III (SYTIII).
2.0e-08:102:35
MUS MUSCULUS (MOUSE).
035681
- 15 F-THYRO1001128
GLYCOPROTEIN X PRECURSOR.
6.8e-07:182:31
EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).
P28968
- 20 F-THYRO1001205
NEUROGRANIN (NG) (PROTEIN KINASE C SUBSTRATE 7.5 KD PROTEIN) (RC3).
0.91:33:42
RATTUS NORVEGICUS (RAT).
Q04940
- 25 F-THYRO1001237
HYPOTHETICAL PROTEIN IN NIFH2 3 REGION (FRAGMENT).
4.0e-07:68:38
METHANOCOCCUS THERMOLITHOTROPHICUS.
P05410
- 30 F-THYRO1001242
SYNAPSINS IA AND IB (BRAIN PROTEIN 4.1).
1.0:104:35
HOMO SAPIENS (HUMAN).
35 P17600
- 40 F-THYRO1001266
SODIUM/GLUCOSE COTRANSPORTER 1 (NA(+)/GLUCOSE COTRANSPORTER 1) (HIGH AFFINITY SODI-
UM-GLUCOSE COTRANSPORTER).
4.3e-09:119:27
ORYCTOLAGUS CUNICULUS (RABBIT).
P11170
- 45 F-THYRO1001327
HYPOTHETICAL 23.7 KD PROTEIN IN CYR1-OST1 INTERGENIC REGION.
1.7e-06:141:24
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P41544
- 50 F-THYRO1001456
HYPOTHETICAL 56.2 KD PROTEIN CY31.25C.
1.1e-11:88:48
MYCOBACTERIUM TUBERCULOSIS.
Q10555
- 55 F-THYRO1001457
PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).
2.1e-68:228:59

HOMO SAPIENS (HUMAN).
Q15139

5 F-THYRO1001471
COLLAGEN 1(X) CHAIN PRECURSOR.
3.9e-05:204:30
GALLUS GALLUS (CHICKEN).
P08125

10 F-THYRO1001478
COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.
0.038:162:31
HOMO SAPIENS (HUMAN).
Q03692

15 F-THYRO1001495
!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!
4.8e-19:50:82
HOMO SAPIENS (HUMAN).
20 P39193

F-THYRO1001523
!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!
5.0e-13:66:62
25 HOMO SAPIENS (HUMAN).
P39195

F-THYRO1001529
SERINE PALMITOYLTRANSFERASE 2 (EC 2.3.1.50) (LONG CHAIN BASE BIOSYNTHESIS PROTEIN 2) (SPT
30 2).
1.6e-27:115:53
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
Q09925

35 F-THYRO1001593
PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).
3.3e-92:225:77
HOMO SAPIENS (HUMAN).
P27448

40 F-THYRO1001608
PROLINE-RICH PROTEIN MP-2 PRECURSOR.
1.2e-07:127:35
MUS MUSCULUS (MOUSE).
45 P05142

F-THYRO1001641
NUC-1 NEGATIVE REGULATORY PROTEIN PREG.
0.0039:98:31
50 NEUROSPORA CRASSA.
Q06712

F-THYRO1001700
INTERFERON-INDUCED, DOUBLE-STRANDED RNA-ACTIVATED PROTEIN KINASE (EC 2.7.1.-) (INTERFER-
55 ON-INDUCIBLE RNA-DEPENDENT PROTEIN KINASE) (P68 KINASE) (P1/EIF-2A PROTEIN KINASE).
3.3e-09:65:43
HOMO SAPIENS (HUMAN).
P19525

- 5 F-THYRO1001702
MYELOID UPREGULATED PROTEIN.
7.8e-62:161:78
MUS MUSCULUS (MOUSE).
035682
- 10 F-THYRO1001725
PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENTS).
0.00061:82:41
RATTUS NORVEGICUS (RAT).
P20468
- 15 F-THYRO1001770
PROBABLE SERINE/THREONINE-PROTEIN KINASE YNL020C (EC 2.7.1.-).
1.0e-20:165:35
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P53974
- 20 F-THYRO1001803
GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-
GLUCAN GLUCOHYDROLASE).
3.6e-07:221:30
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P08640
- 25 F-Y79AA1000030
TRANSCRIPTIONAL ACTIVATOR FE65.
4.5e-09:43:46
RATTUS NORVEGICUS (RAT).
30 P46933
- F-Y79AA1000127
FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL).
1.3e-05:72:43
35 HOMO SAPIENS (HUMAN).
P48023
- F-Y79AA1000207
STANNIOCALCIN PRECURSOR (STC) (CORPUSCLES OF STANNIUS PROTEIN) (CS) (HYPOCALCIN) (TEL-
EOCALCIN).
40 1.0:100:27
ANGUILLA AUSTRALIS (AUSTRALIAN EEL).
P18301
- 45 F-Y79AA1000226
HYPOTHETICAL 52.8 KD PROTEIN T05E11.5 IN CHROMOSOME IV.
2.6e-07:188:28
CAENORHABDITIS ELEGANS.
P49049
- 50 F-Y79AA1000270
VACUOLAR ATP SYNTHASE SUBUNIT AC45 PRECURSOR (EC 3.6.1.34) (V-ATPASE AC45 SUBUNIT).
1.6e-102:233:87
BOS TAURUS (BOVINE).
55 P40682
- F-Y79AA1000426
INHIBIN BETA C CHAIN PRECURSOR (ACTIVIN BETA-C CHAIN).

- 1.1e-14:149:38
HOMO SAPIENS (HUMAN).
P55103
- 5 F-Y79AA1000521
MALE SPECIFIC SPERM PROTEIN MST84DD.
0.00079:60:36
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q01645
- 10 F-Y79AA1000750
EBNA-1 NUCLEAR PROTEIN.
2.0e-09:131:38
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03211
- 15 F-Y79AA1000776
CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER)
(SPRP).
20 0.080:44:40
SUS SCROFA (PIG).
P35323
- F-Y79AA1000777
25 PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).
4.2e-33:204:39
THERMOMONOSPORA CURVATA.
P49695
- 30 F-Y79AA1000876
PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1) (PROLYL 4-HYDROXYLASE BETA SUB-
UNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55).
4.6e-16:115:38
BOS TAURUS (BOVINE).
35 P05307
- F-Y79AA1000888
TRNA PSEUDOURIDINE SYNTHASE A (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE I) (PSEUDOURIDINE
SYNTHASE I) (URACIL HYDROLYASE).
40 2.0e-09:159:35
TREPONEMA PALLIDUM.
083802
- F-Y79AA1000959
45 HOMEODOMAIN PROTEIN HOX-B3 (HOX-2.7) (MH-23).
8.8e-08:72:38
MUS MUSCULUS (MOUSE).
P09026
- 50 F-Y79AA1000967
CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).
1.1e-37:202:42
RATTUS NORVEGICUS (RAT).
Q63450
- 55 F-Y79AA1001013
SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS : PEPTIDE P-D] (FRAGMENT).
0.038:128:28

HOMO SAPIENS (HUMAN).
P10162

5 F-Y79AA1001056
HYPOTHETICAL 7.1 KD PROTEIN IN TK-VS INTERGENIC REGION.
0.41:42:30
BACTERIOPHAGE T4.
P13307

10 F-Y79AA1001062
TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).
9.9e-13:132:38
HOMO SAPIENS (HUMAN).
Q13829

15 F-Y79AA1001090
ANKYRIN HOMOLOG PRECURSOR.
4.0e-19:176:34
CHROMATIUM VINOSUM.
20 Q06527

F-Y79AA1001212
HYPOTHETICAL PROTEIN MJ0110.
0.095:55:34
25 METHANOCOCCUS JANNASCHII.
Q57574

F-Y79AA1001264
HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR.
30 3.3e-53:177:55
CAENORHABDITIS ELEGANS.
Q10005

F-Y79AA1001272
35 ACROSIN PRECURSOR (EC 3.4.21.10).
6.3e-08:78:46
ORYCTOLAGUS CUNICULUS (RABBIT).
P48038

40 F-Y79AA1001328
DELTA-LIKE PROTEIN 1 PRECURSOR (DELTA1).
1.3e-08:118:39
RATTUS NORVEGICUS (RAT).
P97677

45 F-Y79AA1001426
BAND 3 ANION TRANSPORT PROTEIN.
1.7e-18:156:32
GALLUS GALLUS (CHICKEN).
50 P15575

F-Y79AA1001427
INDUCIBLE NITRATE REDUCTASE 2 (EC 1.6.6.1) (NR).
1.1e-49:131:51
55 GLYCINE MAX (SOYBEAN).
P39870

F-Y79AA1001430

- 5 RING CANAL PROTEIN (KELCH PROTEIN).
2.5e-24:157:40
DROSOPHILA MELANOGASTER (FRUIT FLY).
Q04652
- 10 F-Y79AA1001523
TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).
6.2e-15:141:39
HOMO SAPIENS (HUMAN).
Q13263
- 15 F-Y79AA1001530
TUBULIN BETA-5 CHAIN.
8.0e-76:204:76
HOMO SAPIENS (HUMAN).
P04350
- 20 F-Y79AA1001592
PTB-ASSOCIATED SPLICING FACTOR (PSF).
0.42:104:33
HOMO SAPIENS (HUMAN).
P23246
- 25 F-Y79AA1001727
AMALGAM PROTEIN PRECURSOR.
1.9e-09:185:28
DROSOPHILA MELANOGASTER (FRUIT FLY).
P15364
- 30 F-Y79AA1001787
PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).
7.6e-43:210:45
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
Q12697
- 35 F-Y79AA1001793
CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).
0.077:44:40
SUS SCROFA (PIG).
P35323
- 45 F-Y79AA1001795
HYPOTHETICAL BHLF1 PROTEIN.
0.00014:210:31
EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).
P03181
- 50 F-Y79AA1001799
MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.
2.8e-18:107:44
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P23500
- 55 F-Y79AA1001803
SECRETOGRANIN III PRECURSOR (SGIII).
1.3e-68:182:76

MUS MUSCULUS (MOUSE).
P47867

5 F-Y79AA1001863
GLYCOPROTEIN J.
0.030:61:32
HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).
P06480

10 F-Y79AA1002022
WISKOTT-ALDRICH SYNDROME PROTEIN (WASP).
9.8e-08:127:37
HOMO SAPIENS (HUMAN).
P42768

15 F-Y79AA1002058
CCAAT/ENHANCER BINDING PROTEIN DELTA (C/EBP DELTA) (NUCLEAR FACTOR NF-IL6-BETA) (NF-IL6-BETA).
0.28:56:42
20 HOMO SAPIENS (HUMAN).
P49716

F-Y79AA1002121
D-BINDING PROTEIN (DBP) (ALBUMIN D BOX-BINDING PROTEIN).
25 0.71:57:36
MUS MUSCULUS (MOUSE).
Q60925

F-Y79AA1002129
30 TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).
0.98:158:24
PSEUDOMONAS AERUGINOSA.
P15276

35 F-Y79AA1002213
HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III.
4.7e-39:218:41
CAENORHABDITIS ELEGANS.
Q03567

40 F-Y79AA1002334
HYPOTHETICAL PROTEIN MJ1345.
1.8e-08:164:26
METHANOCOCCUS JANNASCHII.
45 Q58741

F-Y79AA1002373
CORNIFIN (SMALL PROLINE-RICH PROTEIN I) (SPR-I) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER)
(SPRP).
50 0.083:44:40
SUS SCROFA (PIG).
P35323

F-Y79AA1002376
55 DYNEIN INTERMEDIATE CHAIN 2, CYTOSOLIC (DH IC-2).
3.0e-91:214:83
RATTUS NORVEGICUS (RAT).
Q62871

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F-Y79AA1002378
ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCRIPTION FACTOR RU49).
1.0e-59:163:74
MUS MUSCULUS (MOUSE).
Q07231

F-Y79AA1002381
CELL DIVISION CONTROL PROTEIN 28 (EC 2.7.1.-).
9.5e-41:179:38
SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
P00546

Homology search result 6

[0296] The result of the homology search in the GenBank(<http://www.ncbi.nlm.nih.gov/web/GenBank/>) using the clone sequences of the 5'-ends. except EST and STS sequences

Indicated are from the top,
the name of the clone sequence,
definition of the top hit data,
the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
the Accession No. of the top hit data.

[0297] Data were not shown for the clones in which the P-value was higher than 1.

F-BNGH41000020
H.sapiens mitochondrial DNA, complete genome.
6.0e-188:913:97
X93334

F-BNGH41000087
Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene similar to GLU-COSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence.
7.1e-32:176:99
AL034418

F-BNGH41000091
Homo sapiens potassium channel h-eag.
1.6e-79:687:76
AJ001366

F-HEMBA1000006
S.erythraea second and third ORF's of eryA gene, complete cds.
0.95:243:64
M63677

F-HEMBA1000121
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT SE-
QUENCE.
5.9e-70:450:89
AL031291

F-HEMBA1000128
Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-14, complete sequence.
1.0:274:59
Z98549

F-HEMBA1000275

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Herpes simplex virus type 2 (strain HG52), complete genome.
0.036:625:55
Z86099

5 F-HEMBA1000300
Homo sapiens chromosome 17, clone hRPK.178_C_3, complete sequence.
1.4e-40:343:80
AC005702

10 F-HEMBA1000349
Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence.
7.5e-65:451:72
AC005922

15 F-HEMBA1000443
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 222E13, WORKING DRAFT SE-
QUENCE.
8.1e-77:216:95
Z93241

20 F-HEMBA1000462
Caenorhabditis elegans cosmid C49H3.
3.7e-06:98:82
U42436

25 F-HEMBA1000477
Mus musculus BALB/c putative growth factor GDF7 (Gdf7) gene, partial cds.
9.1e-05:190:65
U08339

30 F-HEMBA1000590
Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphig-
lycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG
island, complete sequence.
35 3.0e-102:209:99
AL021578

F-HEMBA1000634
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0539L10; HTGS phase 1,
40 WORKING DRAFT SEQUENCE, 15 unordered pieces.
2.0e-95:460:99
AC004480

F-HEMBA1000671
45 Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.
1.5e-28:259:69
AC006116

F-HEMBA1000713
50 Homo sapiens 10kD protein (BC10) mRNA, complete cds.
6.5e-126:442:97
AF053470

F-HEMBA1000732
55 Homo sapiens clone IMAGE Consortium 302831 latent transforming growth factor-beta binding protein 4 mRNA,
partial cds.
1.7e-45:258:94
AF054502

- 5 F-HEMBA1000745
Streptomyces coelicolor cosmid 3F9.
3.5e-06:360:61
AL023862
- 10 F-HEMBA1000835
Homo sapiens fibrillin mRNA, complete cds.
1.3e-07:151:69
L13923
- 15 F-HEMBA1000875
Human Krueppel-type zinc finger protein (ZNF169) gene, partial cds.
2.6e-28:249:81
U28322
- 20 F-HEMBA1000907
Spermatozopsis similis mRNA for 95 kD basal apparatus-protein.
3.4e-09:599:60
AJ001438
- 25 F-HEMBA1000940
Homo sapiens connexin46.6 (Cx46.6) gene, complete cds.
1.7e-16:307:66
AF014643
- 30 F-HEMBA1000962
Homo sapiens Chromosome 11q12.2 PAC clone pDJ519c13 containing human gene for ferritin heavy chain (FTH),
complete sequence.
0.00040:497:59
AC004228
- 35 F-HEMBA1001184
Homo sapiens SH3 domain binding glutamic acid-rich-like protein (SH3BGRL) mRNA, complete cds.
8.8e-23:404:67
AF042081
- 40 F-HEMBA1001221
Human transmembrane protein mRNA, complete cds.
2.4e-42:858:63
U19878
- 45 F-HEMBA1001228
Human germline oligomeric matrix protein (COMP) mRNA, complete cds.
1.9e-82:470:91
L32137
- 50 F-HEMBA1001272
Human Ig gamma-2 heavy chain switch region.
0.032:549:60
U39934
- 55 F-HEMBA1001296
H.sapiens mRNA for PQ-rich protein.
6.9e-07:73:98
Z50194
- F-HEMBA1001297
Homo sapiens putative transcription factor CA150 mRNA, complete cds.

9.3e-14:143:81
AF017789

F-HEMBA1001390

5 Mus musculus polymerase I-transcript release factor mRNA, complete cds.
2.5e-56:464:81
AF036249

F-HEMBA1001563

10 Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo) gene, an unknown putative gene, a pseudogene with high similarity to part of antigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete sequence.
3.1e-06:210:68
15 AL022165

F-HEMBA1001621

Human G protein-coupled receptor APJ gene, complete cds.
2.0e-98:516:95
20 U03642

F-HEMBA1001878

Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds.
1.0e-170:810:98
25 AF090988

F-HEMBA1001886

Human repressor transcriptional factor (ZNF85) mRNA, complete cds.
3.3e-114:849:80
30 U35376

F-HEMBA1002048

HS_3058_B2_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058
Col=22 Row=B, genomic survey sequence.
35 3.8e-11:244:66
AQ103440

F-HEMBA1002131

Homo sapiens mRNA for KIAA0584 protein, partial cds.
3.5e-44:709:66
40 AB011156

F-HEMBA1002163

Homo sapiens chromosome X, clone 592, WORKING DRAFT SEQUENCE, 8 unordered pieces.
45 2.3e-28:373:71
AC002489

F-HEMBA1002164

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SE-
50 QUENCE.
1.3e-127:493:99
AL031427

F-HEMBA1002167

Rattus norvegicus neuroligin I mRNA, complete cds.
8. 1e-155:850:91
55 U22952

- 5 F-HEMBA1002178
Homo sapiens mRNA for KIAA0584 protein, partial cds.
2.6e-46:794:65
AB011156
- 10 F-HEMBA1002195
Human lysosomal alpha-mannosidase (manB) gene, 5' flanking region and exon 1.
7.7e-35:255:86
U60885
- 15 F-HEMBA1002227
Homo sapiens mRNA for 80K-L protein, complete cds.
3.8e-137:382:95
D10522
- 20 F-HEMBA1002239
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-485G10, complete sequence.
4.5e-43:452:74
AC003049
- 25 F-HEMBA1002316
Homo sapiens DNA sequence from PAC 29C18 on chromosome 22.
3.0e-22:609:67
Z97192
- 30 F-HEMBA1002420
Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.
4.2e-142:322:98
AC005632
- 35 F-HEMBA1002421
Human heparan sulfate proteoglycan (HSPG) core protein, 3' end.
1.3e-165:778:98
J04621
- 40 F-HEMBA1002524
Homo sapiens clone UWGC:y55c025 from 6p21, complete sequence.
1.3e-153:313:96
AC004209
- 45 F-HEMBA1002551
Human potential CENP-C binding target sequence, 0.7 kb clone, partial sequence 2.
6.1e-16:108:97
U57994
- 50 F-HEMBA1002767
Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds.
1.4e-168:798:98
AF038660
- 55 F-HEMBA1002985
HS_3165_A2_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
Plate=3165 Col=16 Row=E, genomic survey sequence.
1.7e-08:127:76
AQ142051
- F-HEMBA1002992
RPCI11-67B15.TJ RPCI11 Homo sapiens genomic clone R-67815, genomic survey sequence.

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2.7e-11:119:86
AQ201833

5 F-HEMBA1003047
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.
4.5e-187:873:99
AF034611

10 F-HEMBA1003072
Gallus gallus single-strand DNA-binding protein csdp mRNA, partial cds.
4.1e-50:515:73
U68380

15 F-HEMBA1003101
Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.
5.3e-139:671:98
AF049891

20 F-HEMBA1003120
Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.
3.3e-44:213:73
AC006116

25 F-HEMBA1003230
Homo sapiens UP50 mRNA, complete cds.
5.5e-183:856:98
AF093118

30 F-HEMBA1003294
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 495010, WORKING DRAFT SE-
QUENCE.
4.2e-38:558:69
AL031121

35 F-HEMBA1003315
Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K9I9, complete sequence.
1.2e-61:737:68
AB013390

40 F-HEMBA1003392
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.
2.9e-183:851:99
AF074264

45 F-HEMBA1003399
Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.
8.7e-16:215:74
AC005282

50 F-HEMBA1003487
H.sapiens DNA sequence.
0.0075:158:67
Z22340

55 F-HEMBA1003497
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 2705, WORKING DRAFT SEQUENCE.
1.1e-109:538:98
AL033529

- 5 F-HEMBA1003530
S.scrofa mRNA for BM88 antigen.
2.8e-47:644:69
X82027
- 10 F-HEMBA1003602
Human (lambda) DNA for immunoglobulin light chain.
2.5e-94:551:91
D86997
- 15 F-HEMBA1003732
Homo sapiens clone DJ0935K16, complete sequence.
6.1e-151:777:96
AC006011
- 20 F-HEMBA1003945
Homo sapiens clone 638 unknown mRNA, complete sequence.
1.8e-76:310:93
AF091085
- 25 F-HEMBA1004007
F-HEMBA1004067
Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S
ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG Island, complete sequence.
8.7e-133:718:94
AL031864
- 30 F-HEMBA1004085
Homo sapiens, clone hRPK.2_A_1, complete sequence.
2.7e-58:256:80
AC006197
- 35 F-HEMBA1004110
Homo sapiens intersectin short form mRNA, complete cds.
3.8e-159:779:96
AF064243
- 40 F-HEMBA1004250
Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.
1.2e-183:863:99
AC005752
- 45 F-HEMBA1004391
H.sapiens gene for neural cell adhesion molecule L1.
0.51:426:59
Z29373
- 50 F-HEMBA1004444
Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.
3.3e-147:463:93
AC004938
- 55 F-HEMBA1004454
Homo sapiens tetraspan NET-4 mRNA, complete cds.
0.00036:230:62
AF065389

- 5 F-HEMBA1004505
D.melanogaster mRNA for alpha 1,2 mannosidase.
5.5e-17:663:58
X82640
- 10 F-HEMBA1004785
Gallus gallus mRNA for chromobox protein (CHCB3), complete cds.
6.6e-19:322:68
AB005619
- 15 F-HEMBA1004797
Haemonchus contortus GT microsatellite DNA sequence.
3.0e-08:175:71
U84474
- 20 F-HEMBA1004952
Mus musculus recombinant quaking gene sequence.
4.8e-15:398:65
U44942
- F-HEMBA1004971
- F-HEMBA1004982
- 25 F-HEMBA1005070
Human mRNA for KIAA0310 gene, complete cds.
2.5e-65:370:93
AB002308
- 30 F-HEMBA1005084
Mouse transcriptional control element.
0.0024:189:63
M17284
- 35 F-HEMBA1005145
Pseudorabies virus glycoprotein gp50 gene, complete cds.
0.00022:395:60
AF092447
- 40 F-HEMBA1005230
Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.
2.8e-102:302:94
AC006116
- 45 F-HEMBA1005246
Homo sapiens CAGH44 mRNA, partial cds.
5.0e-29:429:66
U80741
- 50 F-HEMBA1005267
Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.
1.0e-43:320:87
AF042089
- 55 F-HEMBA1005337
Plasmodium falciparum MAL3P6, complete sequence.
4.1e-08:84:89

Z98551

F-HEMBA1005430

5 F-HEMBA1005449
T.aestivum mRNA for a proline-rich protein.
0.00097:385:61
X52472

10 F-HEMBA1005489
Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for creatine transporter (SLC6A8), CDM, adrenoleukodystrophy (ALD), Na⁺-isocitrate dehydrogenase gamma subunit (IDH), and translocon-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq281u1 gene and cytochrome C (CCp) pseudogene.
15 7.8e-16:405:62
U52111

F-HEMBA1005522
O.cuniculus rACNG mRNA for aorta CNG channel.
20 5.9e-47:344:85
X59668

F-HEMBA1005545
Human m3 muscarinic acetylcholine receptor (CHRM3) gene, complete cds.
25 5.1e-173:810:98
U29589

F-HEMBA1005698

30 F-HEMBA1005913
HS_2249_B1_E01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2249
Col=1 Row=J, genomic survey sequence.
0.17:215:61
AQ072649

35 F-HEMBA1005929
Homo sapiens chromosome 19, cosmid R31237, complete sequence.
7.0e-107:285:93
AC005581

40 F-HEMBA1005945
Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier mRNA, complete cds.
1.8e-46:670:65
AF004161

45 F-HEMBA1006016
CIT-HSP-2334L16.TF CIT-HSP Homo Sapiens genomic clone 2334L16, genomic survey sequence.
2.1e-13:246:69
AQ038406

50 F-HEMBA1006171

F-HEMBA1006276
Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.
55 1.4e-144:416:93
AC005261

F-HEMBA1006299

- F-HEMBA1006311
- F-HEMBA1006335
Human DNA sequence from clone 496H19 on chromosome 6q24 Contains ESTs, complete sequence.
5 9.6e-61:370:91
AL023582
- F-HEMBA1006357
Homo sapiens secretory carrier membrane protein (SCAMP2) mRNA, complete cds.
10 2.3e-26:389:67
AF005038
- F-HEMBA1006430
Caenorhabditis elegans cosmid T12A2.
15 4.6e-23:283:72
U13019
- F-HEMBA1006482
Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.
20 1.9e-144:575:98
AF026852
- F-HEMBA1006517
- F-HEMBA1006544
Homo sapiens suppressor of white-apricot homolog 2 (SWAP2) gene, exons 12 and 13.
25 2.3e-151:732:97
AF042809
- F-HEMBA1006572
HS_3058_B2_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058
30 Col=22 Row=B, genomic survey sequence.
1.9e-45:245:96
AQ103440
- F-HEMBA1006658
Homo sapiens mRNA for KIAA0687 protein, partial cds.
35 3.6e-127:646:95
AB014587
- F-HEMBA1006707
Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphig-
lycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG
45 island, complete sequence.
1.7e-118:397:98
AL021578
- F-HEMBA1006724
H.sapiens CpG island DNA genomic Mse1 fragment, clone 40c2, forward read cpg40c2.ft1k.
50 1.4e-53:282:97
Z55440
- F-HEMBA1006749
Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphig-
lycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG
55 island, complete sequence.
3.9e-116:457:98
AL021578

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- F-HEMBA1006770
Xenopus laevis elav-type ribonucleoprotein (etr-1) mRNA, complete cds.
1.6e-53:280:81
U16800
- 5 F-HEMBA1006902
Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.
10 4.9e-122:462:98
AL021578
- F-HEMBA1006912
- 15 F-HEMBA1006916
Homo sapiens Grb14 mRNA, complete cds.
1.6e-118:651:92
L76687
- 20 F-HEMBA1006960
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 110F11, WORKING DRAFT SEQUENCE.
0.20:298:60
AL033526
- 25 F-HEMBA1007013
Rattus norvegicus repeat element associated with the Rasgrf1 gene.
8.0e-07:531:59
AF056927
- 30 F-HEMBA1007057
Human DNA sequence from clone 522J7 on chromosome 22q13.3. Contains part of a 60S Ribosomal protein L5 pseudogene and a Peregrin (BR140) LIKE gene downstream of a putative CpG island. Contains ESTs, STSs and GSSs, complete sequence.
0.27:277:64
35 Z98885
- F-HEMBA1007063
- F-HEMBA1007226
40 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 310013, WORKING DRAFT SEQUENCE.
0.00033:488:63
AL031658
- 45 F-HEMBA1007241
Caenorhabditis elegans cosmid T15B7.
0.068:304:59
AF022985
- 50 F-HEMBA1007291
Homo sapiens chromosome 19, fosmid 37502, complete sequence.
6.2e-123:587:98
AC004755
- 55 F-HEMBA1007332
Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.
1.3e-30:172:97
U56430

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- F-HEMBB1000106
Human DNA sequence from clone 1170D6 on chromosome Xq22.3-23. Contains a pseudogene similar to U-SNRNP-associated Cyclophilin (USA-CYP, EC 5.2.1.8), ESTs, an STS and a GSS, complete sequence.
0.033:332:61
5 AL030995
- F-HEMBB1000276
Dictyostelium discoideum gene encoding a novel glycoprotein.
0.00070:440:60
10 AJ005262
- F-HEMBB1000309
Homo sapiens zinc finger protein (MBLL) mRNA, complete cds.
7.6e-34:180:100
15 AF061261
- F-HEMBB1000407
Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces. 0.16:228:64
AC000384
20
- F-HEMBB1000447
Homo sapiens JWA protein mRNA, complete cds.
1.4e-158:750:98
AF070523
25
- F-HEMBB1000542
Human DNA sequence from PAC 509L4 on chromosome 6q22.1-6q22.33. Contains SSX3 like pseudogene, EST, STS.
4.3e-141:874:89
30 Z99496
- F-HEMBB1000567
Human DNA for insulin-like growth factor II (IGF-2); exon 7 and additional ORF.
9.7e-122:572:99
35 X07868
- F-HEMBB1000642
- F-HEMBB1000668
Caenorhabditis elegans cosmid K06A5.
0.00041:174:64
40 AF039038
- F-HEMBB1000679
C.familiaris mRNA for TRAM-protein.
6.1e-100:756:80
45 X63678
- F-HEMBB1000881
Danio rerio mRNA for MINDIN2, complete cds.
6.2e-40:581:66
50 AB006085
- F-HEMBB1000905
Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.
4.9e-91:209:94
55 AC005089

- 5 F-HEMBB1001026
Human p76 mRNA, complete cds.
1.9e-06:410:61
U81006
- 10 F-HEMBB1001048
Human Hpast (HPAST) mRNA, complete cds.
6.8e-55:524:75
AF001434
- 15 F-HEMBB1001200
Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9
unordered pieces.
4.4e-12:794:59
AC004157
- 20 F-HEMBB1001407
Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1
ordered pieces.
2.7e-43:281:91
AC004150
- 25 F-HEMBB1001530
HS_2255_B1_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens
genomic clone Plate=2255 Col=9 Row=L, genomic survey sequence.
2.1e-14:95:97
AQ131814
- 30 F-HEMBB1001547
S.cerevisiae chromosome VII reading frame ORF YGL236c.
1.1e-19:550:61
Z72758
- 35 F-HEMBB1001573
Homo sapiens 12p13.3 PAC RPCI5-951N9 (Roswell Park Cancer Institute Human PAC library) complete se-
quence.
2.7e-07:467:60
AC004672
- 40 F-HEMBB1001847
H.sapiens CpG island DNA genomic Mse1 fragment, clone 13d12, reverse read cpg13d12.rt1c.
1.1e-14:94:100
Z64565
- 45 F-HEMBB1001959
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SE-
QUENCE.
1.2e-82:492:90
AL034405
- 50 F-HEMBB1001978
Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, complete sequence.
7.0e-23:239:76
AC005386
- 55 F-HEMBB1002039
Human DNA sequence from cosmid 315B17, between markers DXS366 and DXS87 on chromosome X contains
ESTs.

- 3.5e-49:605:71
Z73967
- 5 F-HEMBB1002041
R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).
3.5e-09:501:60
X83546
- 10 F-HEMBB1002051
Homo sapiens E74-like factor 5 (ELF5) mRNA, complete cds.
3.1e-95:454:99
AF049703
- 15 F-HEMBB1002120
- F-HEMBB1002162
Homo sapiens genethonin 1 mRNA, complete cds.
7.0e-67:328:99
AF062534
- 20 F-HEMBB1002228
Homo sapiens unknown mRNA, complete cds.
1.6e-39:208:98
AF047439
- 25 F-HEMBB1002245
Rattus norvegicus prostaglandin F2a receptor regulatory protein precursor, mRNA, complete cds.
3.7e-68:424:87
U26595
- 30 F-HEMBB1002302
RPCI11-18E11.TVB RPCI-11 Homo sapiens genomic clone RPCI-11-18E11, genomic survey sequence.
2.7e-15:101:98
B88081
- 35 F-HEMBB1002427
Homo sapiens chromosome 9q34, clone 70C11, complete sequence.
2.9e-123:249:90
AC002319
- 40 F-HEMBB1002465
Mouse short chain acyl-CoA dehydrogenase mRNA, complete cds.
7.9e-18:545:61
L11163
- 45 F-HEMBB1002661
Drosophila melanogaster; Chromosome 2R; Region 44A1-44A2; P1 clone DS07435, WORKING DRAFT SE-
QUENCE, 2 unordered pieces.
1.9e-07:187:67
AC005445
- 50 F-HEMBB1002663
- 55 F-HEMBB1002693
Homo sapiens full length insert cDNA, clone ZD85G07.
2.1e-20:136:93
AF086462

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F-MAMMA1000046

CIT-HSP-2166017.TF CIT-HSP Homo sapiens genomic clone 2166017, genomic survey sequence.

2.0e-60:345:92

B92334

5

F-MAMMA1000102

Human DNA sequence from cosmid B33F2 on chromosome 22 Contains ESTs.

3.0e-161:766:98

Z79996

10

F-MAMMA1000106

Rat gene for alpha 1B adrenergic receptor, promoter region and partial cds.

0.0025:247:64

D32045

15

F-MAMMA1000118

Canis familiaris beta1 adrenergic receptor (dogbeta1) gene, complete cds.

6.1e-06:545:60

U73207

20

F-MAMMA1000141

Homo sapiens 12q24.2 PAC RPC11-128M12 (Roswell Park Cancer Institute Human PAC library) complete sequence.

1.5e-10:151:78

AC004024

25

F-MAMMA1000204

Homo Sapiens mRNA for LGMD2B protein.

2.1e-166:781:98

AJ007670

30

F-MAMMA1000226

*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B33108; HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.

2.9e-35:188:100

AC004064

35

F-MAMMA1000403

Human vascular addressin MAdCAM-1 mRNA, complete cds.

0.00043:538:59

U82483

40

F-MAMMA1000449

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 317C6, WORKING DRAFT SEQUENCE.

0.090:514:60

Z97651

45

F-MAMMA1000457

H.sapiens mRNA for NADH-cytochrome b5 reductase.

5.5e-36:469:68

Y09501

50

F-MAMMA1000473

Caenorhabditis elegans cosmid B0491, complete sequence.

0.0052:187:64

Z49907

55

F-MAMMA1000496

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- Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.
1.2e-81:318:92
AC004997
- 5 F-MAMMA1000528
P.falciparum complete gene map of plastid-like DNA (IR-B).
0.016:343:58
X95276
- 10 F-MAMMA1000591
Mus musculus UDP-GalNAc:polypeptide N-acetylgalactosaminyltransferase-T3 mRNA, complete cds.
1.2e-24:493:63
U70538
- 15 F-MAMMA1000614
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1,
WORKING DRAFT SEQUENCE, 21 unordered pieces.
7.5e-13:615:60
AC004670
- 20 F-MAMMA1000652
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-116A10, complete sequence.
1.6e-59:451:82
AC004638
- 25 F-MAMMA1000681
Homo sapiens mRNA for putative G-protein coupled receptor, EDG6.
1.2e-32:636:65
AJ000479
- 30 F-MAMMA1000706
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0110D16; HTGS phase 1,
WORKING DRAFT SEQUENCE, 7 unordered pieces.
6.8e-06:428:62
AC004578
- 35 F-MAMMA1000788
HS_3080_A2_B03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080
Col=6 Row=C, genomic survey sequence.
4.9e-35:204:94
AQ128409
- 40 F-MAMMA1000810
Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3.
5.8e-06:246:65
AL022098
- 45 F-MAMMA1000814
Anadara trapezia (alpha 3.15L) hemoglobin alpha-chain (HBA) gene, exons 2 and 3, intron 2, including hypervar-
iable microsatellite polymorphic repeat regions.
1.0e-12:176:75
L25098
- 50 F-MAMMA1000881
Rattus norvegicus serum and glucocorticoid-regulated kinase (sgk) mRNA, complete cds.
2.8e-07:283:63
L01624
- 55

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- 5 F-MAMMA1000986
Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.
1.8e-166:306:99
AF001550
- 10 F-MAMMA1000994
Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.
0.75:260:61
AL021897
- 15 F-MAMMA1001043
H.sapiens mRNA for latent transforming growth factor-beta binding protein (LTBP-2).
0.038:376:60
Z37976
- 20 F-MAMMA1001066
Homo sapiens DNA from chromosome 19-cosmid f24590 containing CAPNS and POL2RI, genomic sequence.
4.4e-15:162:72
AD001527
- 25 F-MAMMA1001094
Homo sapiens clone 243 unknown mRNA, complete sequence.
6.2e-181:844:99
AF091094
- 30 F-MAMMA1001141
Cams familiaris beta1 adrenergic receptor (dogbeta1) gene, complete cds.
1.3e-10:602:59
U73207
- 35 F-MAMMA1001150
M.musculus (Balb/c) mRNA for serine/threonine protein kinase.
7.7e-57:447:67
Z34524
- 40 F-MAMMA1001237
Rattus norvegicus monocarboxylate transporter MCT3 mRNA, complete cds.
1.5e-08:306:65
AF059258
- 45 F-MAMMA1001284
HS_3076_A1_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3076
Col=15 Row=K, genomic survey sequence.
5.2e-53:307:93
AQ120674
- 50 F-MAMMA1001310
1(2)09851 Drosophila melanogaster P lethal line Drosophila melanogaster genomic Sequence recovered from 3'
end of P element, genomic survey sequence.
0.00072:209:66
AQ025672
- 55 F-MAMMA1001344
Fugu rubripes neural cell adhesion molecule L1 homolog (L1-CAM) gene, complete cds; putative protein 1 (PUT1)
gene, partial cds; mitosis-specific chromosome segregation protein SMC1 homolog (SMC1) gene, complete cds;
and calcium channel alpha-1 subunit homolog (CCA1) and putative protein 2 (PUT2) genes, partial cds, complete
sequence.
5.2e-05:164:67

AF026198

F-MAMMA1001418

Human Na⁺/nucleoside cotransporter (hCNT1a) mRNA, complete cds.

6.0e-35:622:63

U62966

F-MAMMA1001532

Homo sapiens PAC clone DJ0728D04, complete sequence.

5.2e-46:538:74

AC004865

F-MAMMA1001609

Homo sapiens chromosome 10 clone CIT-HSP-1240G16 map 10q25.1, complete sequence. 0.00031:592:57

AC005886

F-MAMMA1001615

H.sapiens CpG island DNA genomic MseI fragment, clone 71h9, reverse read cpq71h9.r11a.

1.2e-25:146:99

Z62710

F-MAMMA1001623

Homo sapiens 12q24.2 BAC RPC11-407A16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.

3.9e-69:471:85

AC006065

F-MAMMA1001634

Human DNA sequence from PAC 93C23 on chromosome X. Contains steroid 5-alpha-reductase pseudogene, ESTs and STS.

2.2e-22:228:79

AL008713

F-MAMMA1001893

HS_3067_B2_H09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3067 Col=18 Row=P, genomic survey sequence.

2.5e-29:188:93

AQ138065

F-MAMMA1001901

Human DNA sequence from clone 354J5 on chromosome 6q21-22. Contains pseudogene similar to zinc finger protein (ZPR1), EST, STS, GSS, complete sequence.

2.0e-23:287:71

Z95118

F-MAMMA1001957

Drosophila melanogaster, chromosome 2L, region 21C5-21D1, P1 clone DS07610, complete sequence.

1.5e-14:192:66

AC004573

F-MAMMA1001978

Human immunoglobulin S(u) like sequence.

0.60:150:66

X15517

F-MAMMA1002070

Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.

3.9e-116:250:93

AC002073

F-MAMMA1002080

Mus musculus chromosome 11, clone mCIT.268_P_23, complete sequence.

1.1e-59:493:78

AC004807

F-MAMMA1002087

HS-1047-B2-A09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830

Col=18 Row=B, genomic survey sequence.

2.1e-31:174:98

B38457

F-MAMMA1002091

Homo sapiens CD39L2 (CD39L2) mRNA, complete cds.

1.6e-156:743:98

AF039916

F-MAMMA1002095

Rat alternatively spliced mRNA.

4.9e-126:691:91

M93017

F-MAMMA1002128

Mus musculus C2C12 unknown mRNA, partial cds.

5.0e-41:353:77

U31629

F-MAMMA1002142

F-MAMMA1002165

Homo sapiens connective tissue growth factor related protein WISP-2 (WISP2) mRNA, complete cds.

1.2e-34:219:90

AF100780

F-MAMMA1002205

Homo Sapiens Chromosome X clone bWXD691, complete sequence.

8.1e-33:535:67

AC004386

F-MAMMA1002224

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 229A8, WORKING DRAFT SEQUENCE.

1.2e-31:274:82

Z86090

F-MAMMA1002234

Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).

9.8e-145:736:91

X53744

F-MAMMA1002586

Drosophila melanogaster cosmid clone 86E4.

0.0071:306:58

AL021086

F-MAMMA1002633

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 850H21, WORKING DRAFT SE-
QUENCE.

- 3.9e-33:297:79
AL031680
- 5 F-MAMMA1003126
Human Hpast (HPAST) mRNA, complete cds.
1.7e-82:801:74
AF001434
- 10 F-NT2RM1000407
Cloning vector pUC-GM-INT, complete sequence.
9.4e-141:673:98
AF025392
- 15 F-NT2RM1000462
, complete sequence.
1.5e-86:232:82
AC005300
- 20 F-NT2RM1000542
Mouse beta-galactosidase (BGAL) gene, complete cds.
4.4e-17:468:62
M57734
- 25 F-NT2RM1000580
Caenorhabditis elegans cosmid F09E5.
1.6e-08:352:61
U37429
- 30 F-NT2RM1000789
Homo sapiens mRNA for hTCF-4.
1.1e-94:299:92
Y11306
- 35 F-NT2RM1000855
Canis familiaris sec61 homologue mRNA, complete cds.
6.6e-110:671:87
M96629
- 40 F-NT2RM1000858
tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].
2.0e-65:716:70
S70011
- 45 F-NT2RM1000899
S.pombe chromosome I cosmid c8C9.
0.0010:300:59
Z99168
- 50 F-NT2RM2000241
Homo sapiens chromosome 12p13.3 clone RPC111-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.
0.99:201:65
AC005844
- 55 F-NT2RM2000306
Homo sapiens DNA sequence from PAC 257I20 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D), TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.
1.1e-142:595:97

AL021878

- 5 F-NT2RM2000410
S.gregaria Abd-B gene.
0.076:172:66
X69161
- 10 F-NT2RM2000423
Arthrobacter sp. beta-galactosidase gene, complete cds.
4.2e-06:606:57
U78028
- 15 F-NT2RM2000497
Homo sapiens chromosome 17, clone hRPK.215_P_18, complete sequence.
1.2e-55:285:81
AC005969
- 20 F-NT2RM2000514
- F-NT2RM2000565
Caenorhabditis elegans cosmid F28C5, complete sequence.
4.2e-18:539:62
Z68315
- 25 F-NT2RM2000582
P.zebra microsatellite locus DNA, 429bp.
0.00015:160:69
X99784
- 30 F-NT2RM2000589
Bos taurus myosin X, complete cds.
3.4e-139:817:88
U55042
- 35 F-NT2RM2000622
H.sapiens MFH-1 gene.
0.0010:466:57
Y08223
- 40 F-NT2RM2000632
Homo sapiens mRNA for TBP-associated factor 170 (TAFII170).
0.0052:331:59
AJ001017
- 45 F-NT2RM2000773
Oryctolagus cuniculus serum amyloid A-activating factor SAF-8 mRNA, partial cds.
2.9e-91:496:93
AF076786
- 50 F-NT2RM2001126
Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds.
1.6e-161:663:99
AF093419
- 55 F-NT2RM2001558
Homo sapiens protein kinase A binding protein AKAP110 mRNA, complete cds.
1.2e-164:770:98
AF093408

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F-NT2RM2001626
 F.rubripes GSS sequence, clone 060E22bA4, genomic survey sequence.
 4.5e-46:606:68
 Z88651
 5

F-NT2RM2001643
 HS-1053-B2-E09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT775
 Col=18 Row=J, genomic survey sequence.
 2.5e-06:181:66
 B41504
 10

F-NT2RM2001738
 S.capreolus ard2 gene and orf2, orf4 and orf5.
 0.41:273:63
 Y11036
 15

F-NT2RM2001767
 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50O24, WORKING DRAFT SEQUENCE.
 8.0e-18:130:92
 AL034380
 20

F-NT2RM2001792
 Homo sapiens mRNA for serum lectin P35, complete cds.
 2.5e-12:244:67
 D49353
 25

F-NT2RM2001818

F-NT2RM2001902
 Drosophila melanogaster mRNA for p21 activated kinase related protein.
 7.2e-74:683:75
 AJ011578
 30

F-NT2RM2001939
 Human G protein-coupled receptor GPR-NGA gene, complete cds.
 1.4e-140:702:96
 U55312
 35

F-NT2RM2001941
 Human gene for muscarinic acetylcholine receptor HM1.
 6.3e-20:488:62
 X15263
 40

F-NT2RM4000100
 Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.
 7.7e-25:162:74
 AC004827
 45

F-NT2RM4000115
 50

F-NT2RM4000198

F-NT2RM4000284
 Human IgG Fc receptor hFcRn mRNA, complete cds.
 7.3e-37:194:98
 U12255
 55

F-NT2RM4000295

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Streptomyces chrysomallus actinomycin synthetase II (acmB) gene, complete cds.
1.6e-05:642:59
AF047717

5 F-NT2RM4000326
Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.
1.0e-127:340:92
AJ003147

10 F-NT2RM4000417
Oncorhynchus kisutch microsatellite OKi20 DNA.
0.44:144:66
AF055444

15 F-NT2RM4000444
S.salar mRNA for transport-associated protein Tap2A.
1.7e-27:577:62
Z83328

20 F-NT2RM4000587
Homo sapiens chromosome 19, cosmid R28058, complete sequence.
7.7e-16:388:64
AC005615

25 F-NT2RM4000593

F-NT2RM4000648
M.musculus mRNA for K-glypican.
30 1.4e-50:610:70
X83577

F-NT2RM4000761
Human mitochondrial DNA, fragment M1, encoding transfer RNAs, cytochrome oxidase I, and 2 URFs.
35 4.8e-167:787:98
M10546

F-NT2RM4000965
S.scrofa mRNA for calcium release channel (CRC).
40 0.044:356:60
X62880

F-NT2RM4000997

45 F-NT2RM4001321
HS-1053-B2-E09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775
Col=18 Row=J, genomic survey sequence.
1.3e-06:181:67
B41504

50 F-NT2RM4001325
Homo sapiens mRNA for chondroitin 6-sulfotransferase, complete cds.
6.6e-12:384:64
AB012192

55 F-NT2RM4001377
Homo sapiens mRNA for KIAA0638 protein, partial cds.
9.7e-155:719:99

AB014538

F-NT2RM4001735

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 483K16, WORKING DRAFT SE-
QUENCE.

1.3e-162:679:96

AL034374

F-NT2RM4001768

Human HepG2 partial cDNA, clone hrnd3a07m5.

2.7e-52:271:98

D17020

F-NT2RM4001843

F-NT2RM4002352

Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds.

1.4e-155:761:97

AB009462

F-NT2RP1000002

Mouse cAMP-dependent protein kinase beta subunit gene, exon 1.

1.7e-06:252:65

M21096

F-NT2RP1000050

Human HepG2 partial cDNA, clone hmd3g02m5.

7.1e-18:115:97

D17047

F-NT2RP1000181

Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH),
complete sequence.

4.2e-139:427:98

AC004228

F-NT2RP1000239

Homo sapiens clone DT1P1E11 mRNA, CAG repeat region.

1.4e-90:524:91

U92989

F-NT2RP1000261

Homo sapiens hPMS1 gene, promoter region and exon 1.

2.5e-14:132:85

AB006462

F-NT2RP1000271

Homo sapiens DNA-binding protein mRNA, complete cds.

4.3e-139:678:97

AF038951

F-NT2RP1000300

Homo sapiens, complete sequence.

0.012:146:69

AC005854

F-NT2RP1000325

H.sapiens gene for phosphate carrier.

- 4.2e-110:438:98
X77337
- 5 F-NT2RP1000448
Streptomyces coelicolor cosmid 1A6.
0.79:209:61
AL023496
- 10 F-NT2RP1000465
Mus musculus nuclear protein NIP45 mRNA, complete cds.
2.2e-29:489:68
U76759
- 15 F-NT2RP1000468
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SE-
QUENCE.
1.6e-49:306:91
AL034405
- 20 F-NT2RP1000551
Homo sapiens putative interferon-related protein (SM15) mRNA, partial cds.
7.5e-139:742:93
U09585
- 25 F-NT2RP1000579
Human succinate dehydrogenase flavoprotein subunit (SDH) mRNA, complete cds.
3.6e-140:798:91
L21936
- 30 F-NT2RP1000613
Sequence 1 from patent US 5589579.
8.1e-10:468:58
I32995
- 35 F-NT2RP1000679
Homo sapiens chromosome 17, clone hRPC.4_G_17, complete sequence.
1.3e-112:448:89
AC003688
- 40 F-NT2RP1000740
H.sapiens CpG island DNA genomic Mse1 fragment, clone 34a2, reverse read cpg34a2.rt1a.
9.3e-14:211:73
Z60772
- 45 F-NT2RP1000903
HS_2256_B1_E10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2256
Col=19 Row=J, genomic survey sequence.
9.0e-21:197:84
AQ084622
- 50 F-NT2RP1000981
F-NT2RP1001004
Danio rerio mRNA for MINDIN2, complete cds.
4.1e-22:472:63
AB006085
- 55 F-NT2RP1001020
Mus musculus clone OST66, genomic survey sequence.

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- 1.5e-47:352:81
AF046696
- 5 F-NT2RP1001031
CIT-HSP-2330P23.TR CIT-HSP Homo sapiens genomic clone 2330P23, genomic survey sequence.
8.0e-26:145:99
AQ035969
- 10 F-NT2RP1001563
Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces. 0.096:405:59
AC004971
- 15 F-NT2RP2000092
Human zinc finger protein ZNF136.
1.8e-54:652:70
U09367
- 20 F-NT2RP2000178
Streptomyces coelicolor cosmid 3F9.
0.92:217:64
AL023862
- 25 F-NT2RP2000240
Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.
2.9e-96:534:90
AF001550
- 30 F-NT2RP2000394
Gallus gallus p52 pro-apototic protein mRNA, complete cds.
2.9e-19:380:65
AF029071
- 35 F-NT2RP2000447
Homo sapiens clone DJ1129D05, complete sequence.
1.3e-109:289:98
AC005630
- 40 F-NT2RP2000479
Human DNA sequence from PAC 130G2 on chromosome 6p22.2-22.3. Contains ribosomal protein L29 pseudo-
gene, ESTs and STSs.
0.0039:219:63
AL008627
- 45 F-NT2RP2000514
Homo sapiens roundabout 2 (robo2) mRNA, partial cds.
3.7e-89:461:95
AF040991
- 50 F-NT2RP2000533
Mus musculus cornichon mRNA, complete cds.
1.4e-113:677:89
AF022811
- 55 F-NT2RP2000610
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SE-
QUENCE.
4.3e-25:177:89
AL034405

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- 5 F-NT2RP2000616
RPC111-75J11.TK MCI11 Homo sapiens genomic clone R-75J11, genomic survey sequence.
8.4e-34:135:91
AQ268877
- 10 F-NT2RP2000649
Homo sapiens CAAX prenyl protease (STE24) mRNA, complete cds.
1.2e-165:802:97
AF064867
- 15 F-NT2RP2000663
Human DNA sequence from cosmid U61B11, between markers DXS366 and DXS87 on chromosome X contains
ESTs.
1.6e-106:365:97
Z73913
- 20 F-NT2RP2000694
Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.
4.2e-112:561:96
AJ012159
- 25 F-NT2RP2000712
HS_3071_A2_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
Plate=3071 Col=10 Row=G, genomic survey sequence.
7.6e-78:389:97
AQ166085
- 30 F-NT2RP2000739
Human mRNA for KIAA0326 gene, partial cds.
6.4e-24:574:62
AB002324
- 35 F-NT2RP2000818
Drosophila melanogaster, chromosome 2R, region 38A5-38B4, BAC clone BACR48M05, complete sequence.
0.00047:304:61
AC005719
- 40 F-NT2RP2000903
Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.
2.6e-110:541:97
AJ012159
- 45 F-NT2RP2001200
Homo sapiens mRNA for KIAA0676 protein, partial cds.
3.3e-1 10:540:96
AB014576
- 50 F-NT2RP2001223
HS-1054-B2-C02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 776
Col=4 Row=F, genomic survey sequence.
7.2e-10:128:77
B41982
- 55 F-NT2RP2001276
Mouse regulatory protein (npdc-1) mRNA, complete cds.
1.2e-38:296:81
L03814

F-NT2RP2001388
 RPCI11-30G23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-30G23, genomic survey sequence.
 0.32:53:94
 B87787

5

F-NT2RP2001469
 M.musculus tex292 mRNA (5'region).
 4.2e-10:120:83
 X80434

10

F-NT2RP2001480
 Homo sapiens thrombospondin 3 (THBS3) gene, complete cds.
 9.0e-140:686:96
 L38969

15

F-NT2RP2001495
 Human transporter protein (g17) mRNA, complete cds.
 1.9e-35:581:64
 U49082

20

F-NT2RP2001514
 Drosophila melanogaster DNA sequence (P1 DS06882 (D310)), complete sequence.
 3.7e-22:475:62
 AC005115

25

F-NT2RP2001529
 Homo sapiens mRNA for ZIP-kinase, complete cds.
 4.6e-152:757:96
 AB007144

30

F-NT2RP2001538
 Sequence 11 from patent US 5624818.
 1.4e-88:528:88
 I41141

35

F-NT2RP2001562
 Homo sapiens GLE1 (GLE1) mRNA, complete cds.
 2.3e-117:572:97
 AF058922

40

F-NT2RP2001662
 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.
 6.1e-107:365:91
 AL031662

45

F-NT2RP2001755
 Sequence 9 from patent US 5750502.
 1.5e-53:518:75
 AR007441

50

F-NT2RP2001769
 A.sativa Aspk11 mRNA.
 4.7e-17:537:60
 X79992

55

F-NT2RP2001817
 Candida albicans SIR2 (SIR2) gene, complete cds.
 4.6e-10:285:61

AF045774

F-NT2RP2001878

Mus musculus repeat element upstream of the Rasgrf1/Cdc25Mm gene.

5.0e-06:554:60

AF021791

F-NT2RP2001903

M.musculus mRNA for m-calpain.

3.1e-06:337:60

Y10139

F-NT2RP2001915

Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.

6.8e-28:488:65

AC005670

F-NT2RP2001921

Homo sapiens clone NH0332L11, complete sequence.

1.1e-77:148:99

AC005538

F-NT2RP2001948

Sequence 2 from patent US 5541311.

0.59:284:57

I24091

F-NT2RP2001956

Feline c-sis proto-oncogene, segment 4.

0.99:101:69

M25356

F-NT2RP2002015

HS-1053-B2-E09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775

Col=18 Row=J, genomic survey sequence.

3.0e-06:181:65

B41504

F-NT2RP2002063

Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.

1.3e-108:418:94

AC004050

F-NT2RP2002188

Rattus norvegicus neuroligin 3 mRNA, complete cds.

1.0e-125:700:90

U41663

F-NT2RP2002232

F-NT2RP2002304

Human FMR1 gene, 5' end.

0.12:93:67

L19476

F-NT2RP2002409

Myxococcus xanthus response regulator FrzZ (frzZ) gene, partial cds; alanine dehydrogenase (aldA), putative ECF sigma factor RpoE1 (rpoE1), and response regulator homolog (frzS) genes, complete cds; and unknown

- genes.
9.0e-10:553:59
AF049107
- 5 F-NT2RP2002510
Mus musculus (129SV) DNA, unmapped BAC 10817, complete sequence.
4.2e-27:573:62
AC004093
- 10 F-NT2RP2002527
Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.
3.2e-110:439:99
AC004228
- 15 F-NT2RP2002533
Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete cds.
6.4e-141:726:95
20 AF040709
- F-NT2RP2002564
Homo sapiens PAC clone DJ0979P20 from 7q33-q35, complete sequence.
2.6e-112:403:98
25 AC004941
- F-NT2RP2002674
HS_3122_B2_A02_MRCIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3122 Col=4 Row=B, genomic survey sequence.
4.8e-13:86:100
30 AQ182907
- F-NT2RP2002721
- 35 F-NT2RP2002824
Arabidopsis thaliana BAC T19D16 genomic sequence.
1.3e-12:135:69
U95973
- 40 F-NT2RP2002942
Homo sapiens mRNA for KIAA0806 protein, complete cds.
6.1e-145:758:94
AB018349
- 45 F-NT2RP2002974
Mus musculus mRNA for Six5, partial cds.
8.0e-84:588:82
D83146
- 50 F-NT2RP2002976
H.sapiens gene for phospholipase C beta 3, exon 14.
0.93:210:61
Z37557
- 55 F-NT2RP2003042
G.gallus mRNA for lecithin-cholesterol acyltransferase.
9.1e-26:462:65
X91011

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F-NT2RP2003138
 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.
 3.9e-142:702:96
 AL031662
 5

F-NT2RP2003179
 Homo sapiens mRNA for KIAA0537 protein, complete cds.
 3.3e-42:587:70
 AB011109
 10

F-NT2RP2003210
 Mus musculus fatty acid transport protein 4 mRNA, partial cds.
 2.6e-112:726:85
 AF072759
 15

F-NT2RP2003302
 Human zinc finger protein ZNF136.
 5.5e-63:691:69
 U09367
 20

F-NT2RP2003369
 Homo sapiens chromosome 7q22 sequence, complete sequence.
 2.0e-49:249:95
 AF053356
 25

F-NT2RP2003383
 Homo sapiens chromosome 1 atrophin-1 related protein (DRPLA) mRNA, complete cds.
 1.5e-159:817:95
 AF016005
 30

F-NT2RP2003390
 Homo sapiens SEC63 (SEC63) mRNA, complete cds.
 7.0e-115:554:98
 AF100141
 35

F-NT2RP2003469
 Genomic sequence from Human 9q34, complete sequence.
 5.6e-38:210:97
 AC001644
 40

F-NT2RP2003545
 Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.
 2.2e-48:579:71
 AF024636
 45

F-NT2RP2003593
 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 971N18, WORKING DRAFT SE-
 QUENCE.
 1.8e-90:326:99
 AL021396
 50

F-NT2RP2003599

F-NT2RP2003655
 M.musculus tex261 mRNA.
 5.3e-77:513:85
 X81058
 55

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- 5 F-NT2RP2003664
Homo sapiens mRNA for leptin receptor gene-related protein.
1.7e-132:630:98
Y12670
- 10 F-NT2RP2003931
Homo sapiens chromosome 19, overlapping cosmids R27918 and R33775, complete sequence.
1.3e-114:411:97
AC004447
- 15 F-NT2RP2003940
Human ZNF43 mRNA.
1.4e-97:693:82
X59244
- 20 F-NT2RP2003950
Sequence 1 from patent US 5648238.
6.9e-13:143:79
I55887
- 25 F-NT2RP2004069
- F-NT2RP2004108
Human zinc finger protein ZNF136.
1.5e-67:548:78
U09367
- 30 F-NT2RP2004141
Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon.
8.0e-10:487:62
U87960
- 35 F-NT2RP2004179
Homo sapiens chromosome 11 from 11p15.5 region, complete sequence.
0.56:600:57
AF015416
- 40 F-NT2RP2004205
Homo sapiens chromosome 16, cosmid clone RT81 (LANL), complete sequence.
0.32:431:55
AC005356
- 45 F-NT2RP2004447
Homo sapiens Chromosome 11q13 BAC Clone 18h3, WORKING DRAFT SEQUENCE, 7 ordered pieces.
2.0e-23:252:79
AC000353
- 50 F-NT2RP2004495
Human transporter protein (g17) mRNA, complete cds.
3.6e-25:497:61
U49082
- 55 F-NT2RP2004524
Genomic sequence from Human 9q34, complete sequence.
5.9e-60:203:98
AC001644
- F-NT2RP2004556

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HS_3022_A1_A11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022
Col=21 Row=A, genomic survey sequence.
1.3e-51:419:79
AQ119143

5

F-NT2RP2004606
cDNA encoding NIC(Natural Inhibitor of Collagenase).
1.2e-113:617:92
E00985

10

F-NT2RP2004648
Felis catus lysosomal beta-galactosidase (Bgal) mRNA, complete cds.
1.5e-15:403:64
AF006749

15

F-NT2RP2004670
Rattus norvegicus vesicla-associate calmodulin-binding protein mRNA, complete cds.
1.1e-73:493:85
L22557

20

F-NT2RP2004794
Mus musculus mRNA for B-IND1 protein.
5.6e-12:109:86
Z97207

25

F-NT2RP2004837
Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.
2.8e-39:352:78
AC006030

30

F-NT2RP2004847
CIT-HSP-2357D24.TR CIT-HSP Homo sapiens genomic clone 2357D24, genomic survey sequence.
2.5e-35:196:96
AQ074738

35

F-NT2RP2005027
Human glucose transporter-like protein-III (GLUT3), complete cds.
2.2e-145:713:96
M20681

40

F-NT2RP2005069
Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.
9.4e-51:200:90
U35245

45

F-NT2RP2005163
Mouse DNA fragment that hybridizes to HSV-1 Smal A fragment.
1.4e-08:231:67
M11041

50

F-NT2RP2005181
Mus musculus cationic amino acid trmsporter (CAT3) mRNA, complete cds.
1.6e-96:575:85
U70859

55

F-NT2RP2005247
Mus musculus ret finger protein mRNA, complete cds.
1.8e-13:310:66

L46855

F-NT2RP2005378

RPCI11-21D23.TP RPCI-11 Homo sapiens genomic clone RPCI-11-21D23, genomic survey sequence.

3.0e-12:131:80

B85846

F-NT2RP2005391

S.muris mRNA for microneme antigen.

2.5e-10:345:61

Z26947

F-NT2RP2005425

Homo sapiens mRNA for KIAA0803 protein, partial cds.

1.0e-116:566:97

AB018346

F-NT2RP2005463

F-NT2RP2005514

F-NT2RP2005535

Homo sapiens DNA-binding protein mRNA, complete cds.

2.3e-125:726:90

AF038951

F-NT2RP2005541

CIT-HSP-2386E2.TF.1 CIT-HSP Homo sapiens genomic clone 2386E2, genomic survey sequence.

6.2e-20:152:88

AQ240341

F-NT2RP2005597

D.melanogaster mRNA for rotated abdomen protein.

0.088:270:57

X95956

F-NT2RP2005632

Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds.

2.0e-07:207:67

U47276

F-NT2RP2005666

Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE, 9 unordered pieces.

1.0:328:57

AC005849

F-NT2RP2005774

Human zinc finger protein ZNF136.

4.0e-44:451:74

U09367

F-NT2RP2005878

Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.

5.1e-16:382:63

AF064635

F-NT2RP2005883

Human DNA sequence from clone 248E1 on chromosome 6q23.1-23.3 Contains DOPAMINE-BETA-MONOOXY-

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GENASE PRECURSOR, EF-1-ALPHA-2 pseudogene EST GSS and CA repeat, complete sequence.
1.5e-30:191:95
AL023578

5 F-NT2RP2005887
Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.
1.8e-50:394:79
AC006030

10 F-NT2RP2005941
Human DNA sequence from cosmid CFAT5, chromosome region 11p13 contains PAX6 exons 1-4, EST and CpG Islands.
9.5e-93:468:96
Z95332

15 F-NT2RP2005994
Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.
1.6e-139:692:96
AC004050

20 F-NT2RP2006004
CIT-HSP-2366J21.TF CIT-HSP Homo sapiens genomic clone 2366J21, genomic survey sequence.
6.6e-39:206:98
AQ080257

25 F-NT2RP2006042
Human mRNA for KIAA0144 gene, complete cds.
1.7e-10:220:69
D63478

30 F-NT2RP2006092
Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.
3.6e-121:562:82
AC005214

35 F-NT2RP2006099
Human Chromosome 11 pac pDJ392a17, complete sequence.
8.7e-76:383:92
AC000385

40 F-NT2RP2006134
Homo sapiens Chromosome 22q11.2 Cosmid Clone 91c In DGCR Region, complete sequence. 0.055:125:71
AC000091

45 F-NT2RP2006269
D.melanogaster mRNA for rotated abdomen protein.
5.4e-05:357:58
X95956

50 F-NT2RP2006512
Sequence 1 from Patent EP 0285405.
3.7e-102:659:85
I05465

55 F-NT2RP3000011
RPC111-43E12.TJ RPC111 Homo sapiens genomic clone R-43E12, genomic survey sequence.
1.8e-10:113:84
AQ195722

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- F-NT2RP3000022
Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isolog of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence.
5 6.7e-116:284:99
AL031178
- F-NT2RP3000059
R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).
10 0.0031:511:59
X83546
- F-NT2RP3000063
Homo sapiens chromosome 19, fosmid 37502, complete sequence.
15 0.20:544:57
AC004755
- F-NT2RP3000125
HS_3025_A1_D11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3025 Col=21 Row=G, genomic survey sequence.
20 1.0e-21:161:88
AQ101452
- F-NT2RP3000148
Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.
25 5.2e-40:257:77
AC002310
- F-NT2RP3000169
Homo sapiens MRS1 mRNA, complete cds.
30 3.4e-106:501:99
AF093239
- F-NT2RP3000171
Mus musculus mRNA for B-IND1 protein.
35 1.8e-97:571:89
Z97207
- F-NT2RP3000172
Rattus norvegicus vesicla-associate calmodulin-binding protein mRNA, complete cds.
40 2.0e-123:702:86
L22557
- F-NT2RP3000201
Homo sapiens mRNA for KIAA0687 protein, partial cds.
45 9.2e-170:792:98
AB014587
- F-NT2RP3000232
HS_3238_B2_D04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=8 Row=H, genomic survey sequence.
50 9.2e-24:174:88
AQ219879
- F-NT2RP3000304
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.
55 3.3e-171:797:98
AF074264

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- 5 F-NT2RP3000378
Mus musculus (clone pVZmSin3A9) mSin3A9 mRNA, complete cds.
5.8e-137:774:89
L38621
- 10 F-NT2RP3000427
Mouse cAMP-dependent protein kinase beta subunit gene, exon 1.
1.5e-18:390:65
M21096
- 15 F-NT2RP3000436
cDNA encoding a human novel protein disulfide isomerase like enzyme,EP52.
4.5e-05:353:59
E13330
- 20 F-NT2RP3000444
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 117715, WORKING DRAFT SEQUENCE.
9.7e-75:203:97
AL022315
- 25 F-NT2RP3000460
Canis familiaris sec61 homologue mRNA, complete cds.
7.1e-131:643:88
M96629
- 30 F-NT2RP3000481
Homo sapiens RanBP7/importin 7 mRNA, complete cds.
1.7e-162:770:98
AF098799
- 35 F-NT2RP3000616
Homo sapiens KIAA0405 mRNA, complete cds.
4.7e-31:579:62
AB007865
- 40 F-NT2RP3000645
Human chromosome 12p13 sequence, complete sequence.
5.9e-07:484:61
U47924
- 45 F-NT2RP3000652
Human ZNF43 mRNA.
4.4e-131:853:84
X59244
- 50 F-NT2RP3000676
Homo sapiens mRNA for KIAA0446 protein, complete cds.
2.7e-86:420:98
AB007915
- 55 F-NT2RP3000677
Human estrogen receptor-related protein (variant ER from breast cancer) mRNA, complete cds.
2.9e-21:125:100
M69296
- F-NT2RP3000721
HS_2221_A2_C01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2221
Col=2 Row=E, genomic survey sequence.

- 0.94:254:60
AQ253443
- 5 F-NT2RP3000789
Mus musculus coding region determinant binding protein mRNA, complete cds.
5.4e-139:827:87
AF061569
- 10 F-NT2RP3000818
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 94M16, WORKING DRAFT SEQUENCE.
3.0e-28:218:86
Z97201
- 15 F-NT2RP3000820
Mus musculus WSB-1 mRNA, complete cds.
1.1e-77:477:87
AF033186
- 20 F-NT2RP3000838
Homo sapiens mRNA for KIAA0638 protein, partial cds.
2.6e-77:682:79
AB014538
- 25 F-NT2RP3000871
Homo sapiens retinoblastoma-interacting protein (RBBP8) mRNA, complete cds.
5.8e-07:350:60
AF043431
- 30 F-NT2RP3000907
Drosophila melanogaster DNA sequence (P1 DS06882 (D310)), complete sequence.
1.7e-13:330:62
AC005115
- 35 F-NT2RP3000921
cDNA GA3-43 encoding novel polypeptide which appear when differentiate from embryo-tumor cell P19 to nerve cell.
6.8e-68:812:69
E12950
- 40 F-NT2RP3001012
cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).
2.4e-129:692:92
E12829
- 45 F-NT2RP3001044
Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.
3.7e-60:393:79
AC006030
- 50 F-NT2RP3001061
F.rubripes GSS sequence, clone 154E17aC12, genomic survey sequence.
1.8e-07:239:62
AL018519
- 55 F-NT2RP3001159
Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.
4.4e-24:156:72

AC004770

F-NT2RP3001170

Homo sapiens mRNA for KIAA0784 protein, partial cds.

2.3e-181:859:98

AB018327

F-NT2RP3001195

Genomic sequence from Human 9q34, complete sequence.

3.8e-53:253:92

AC001644

F-NT2RP3001240

Canis familiaris sec61 homologue mRNA, complete cds.

1.4e-133:740:87

M96629

P-NT2RP3001271

Homo sapiens chromosome 19, cosmid F20237, complete sequence.

0.082:370:60

AC005775

F-NT2RP3001322

Homo sapiens mRNA for KIAA0566 protein, partial cds.

1.9e-38:728:63

AB011138

F-NT2RP3001388

Rattus norvegicus synaptotagmin XI mRNA, complete cds.

1.2e-103:701:83

AF000423

F-NT2RP3001542

Human Chromosome 11 Cosmid cSRL34e5, complete sequence.

8.6e-17:293:65

U73643

F-NT2RP3001560

Mouse mRNA for thymic epithelial cell surface antigen, complete cds.

7.8e-135:742:91

D67067

F-NT2RP3001592

Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.

7.2e-12:188:71

U22398

F-NT2RP3001650

Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.

1.9e-26:374:72

AC005281

F-NT2RP3001685

Homo sapiens 12q13.1 Cosmid C174F5 (Lawrence Livermore LL12NC01 or LL12NC02 human cosmid libraries) complete sequence.

4.6e-73:284:98

AC004550

F-NT2RP3001738

Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.

1.8e-21:186:67

AC004770

F-NT2RP3001754

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.

5.0e-21:131:96

AL034380

F-NT2RP3001858

Homo sapiens mRNA for KIAA0584 protein, partial cds.

5.9e-39:770:63

AB011156

F-NT2RP3001976

M.domesticus (C57B1/6J) mRNA for zinc finger protein 30.

2.0e-37:536:70

Z30174

F-NT2RP3002015

Homo sapiens huntingtin gene, partial exon.

0.024:175:65

L49359

F-NT2RP3002160

Homo sapiens chromosome 9q34, clone 70C11, complete sequence.

1.6e-95:249:91

AC002319

F-NT2RP3002281

Homo sapiens mRNA for KIAA0765 protein, partial cds.

1.6e-149:713:98

AB018308

F-NT2RP3002286

Mus musculus EGF repeat transmembrane protein mRNA, complete cds.

2.0e-136:756:92

U57368

F-NT2RP3002311

Mouse beta-galactosidase (BGAL) gene, complete cds.

1.0e-29:624:63

M57734

F-NT2RP3002324

Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG island.

5.7e-122:655:93

Z69890

F-NT2RP3002342

Human transporter protein (g17) mRNA, complete cds.

9.8e-36:565:65

U49082

F-NT2RP3002353

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Streptomyces phaeochromogenes plasmid pJV1, complete sequence.

0.15:466:60

U23762

5 F-NT2RP3002409

Homo sapiens mRNA for KIAA0719 protein, complete cds.

2.0e-189:897:98

AB018262

10 F-NT2RP3002411

Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.

7.8e-122:796:84

AF064635

15 F-NT2RP3002448

R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).

4.0e-11:403:64

X83546

20 F-NT2RP3002571

Bos taurus mRNA for lyncein.

8.7e-114:652:90

Y17923

25 F-NT2RP3002664

H.sapiens CpG island DNA genomic Mse1 fragment, clone 34a2, reverse read cpg34a2.rt1a.

6.1e-14:211:72

Z60772

30 F-NT2RP3002721

Homo sapiens citrate synthase mRNA, complete cds.

7.5e-179:873:96

AF047042

35 F-NT2RP3002737

Homo sapiens mRNA for HNSPC, complete cds.

1.4e-42:409:75

D82346

40 F-NT2RP3002738

Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds.

8.9e-122:812:83

D29766

45 F-NT2RP3002790

Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.

2.2e-15:626:62

U22398

50 F-NT2RP3002836

Homo sapiens mRNA for KIAA0463 protein, partial cds.

6.8e-152:717:99

AB007932

55 F-NT2RP3002887

R.norvegicus mRNA for leucocyte common antigen-related protein (3941 bp).

2.0e-05:491:59

X83546

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F-NT2RP3002900

Cricetulus griseus COP-coated vesicle membrane protein CHOp24 mRNA, partial cds.

7.3e-13:327:66

U26264

5

F-NT2RP3002958

Mus musculus IgK chain (6S) intron with insertion/deletion mutations.

5.6e-22:403:66

L12153

10

F-NT2RP3002983

Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE.

1.2e-118:339:99

AP000047

15

F-NT2RP3003000

Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds.

7.9e-88:555:88

AF051946

20

F-NT2RP3003076

Streptomyces coelicolor cosmid 2A11.

0.15:505:59

AL031184

25

F-NT2RP3003354

Homo sapiens secretory carrier membrane protein (SCAMP2) mRNA, complete cds.

1.2e-34:625:64

AF005038

30

F-NT2RP3003448

CIT-HSP-721P7.TV CIT-HSP Homo sapiens genomic clone 721P7, genomic survey sequence.

1.2e-16:126:89

B50017

35

F-NT2RP3003469

Homo sapiens chromosome 19, cosmid F23990, complete sequence.

2.0e-18:126:94

AC005262

40

F-NT2RP3003473

Homo sapiens chromosome 17, clone hRPK.1003_J_3, complete sequence.

7. 1e-68:474:71

AC005181

45

F-NT2RP3003527

Homo sapiens mRNA for protein kinase Dyrk1B.

1.4e-160:769:98

Y17999

50

F-NT2RP3003532

Mus musculus cell surface molecule OX-2 mRNA, complete cds.

1.3e-96:712:80

AF004023

55

F-NT2RP3003535

Drosophila melanogaster (P1 DS02368 (D205)) DNA sequence, complete sequence. 0.027:155:65

AC004313

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- 5 F-NT2RP3003559
H.sapiens CpG island DNA genomic Mse1 fragment, clone 171h5, reverse read cpg171h5.rt1a.
3.9e-50:261:97
Z59762
- 10 F-NT2RP3003614
Mus musculus semaphorin Via mRNA, complete cds.
1.7e-131:811:86
AF030430
- 15 F-NT2RP3003729
Homo sapiens chromosome 10 clone LA10NC01_15_E_11 map 10q26.3, WORKING DRAFT SEQUENCE, 3 un-ordered pieces.
1.4e-97:259:91
AC006171
- F-NT2RP3003849
- 20 F-NT2RP3003874
M.musculus mRNA for myosin I heavy chain.
2.9e-151:863:89
X69987
- 25 F-NT2RP3003939
T24C19TF TAMU Arabidopsis thaliana genomic clone T24C19, genomic survey sequence.
1.4e-19:293:68
B29025
- 30 F-NT2RP3003963
CIT-HSP-2050C19.TF CIT-HSP Homo sapiens genomic clone 2050C19, genomic survey sequence.
1.3e-16:111:95
B80539
- 35 F-NT2RP3004000
Homo sapiens klotho gene, exon 1.
0.042:430:60
AB009666
- 40 F-NT2RP3004025
Human DNA sequence from Fosmid 49D8 on chromosome 22, complete sequence.
0.062:197:65
Z82186
- 45 F-NT2RP3004067
Human mRNA for KIAA0375 gene, complete cds.
1.7e-33:556:66
AB002373
- 50 F-NT2RP3004075
jd187 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 5H9, genomic survey sequence.
1.5e-12:438:61
B13419
- 55 F-NT2RP3004083
- F-NT2RP3004090
Dog alpha-L-iduronidase (IDUA) gene, exons 7-12.

1.4e-06:469:60
L01060

F-NT2RP30041 19

5 Human mRNA for KIAA0215 gene, complete cds.
1.3e-72:640:75
D86969

F-NT2RP3004130

10 F-NT2RP3004133
Pseudomonas aeruginosa phage phi CTX DNA, complete genome.
0.0018:421:60
Y13918

F-NT2RP3004202

F-NT2RP3004294
Xenopus laevis ER1 mRNA, complete cds.
20 5.0e-77:335:78
AF015454

F-NT2RP3004309

25 Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete se-
quence.
9.6e-25:231:65
AC004770

F-NT2RP3004321

30 Homo sapiens chromosome 11 from 11p15.5 region, complete sequence.
3.7e-80:279:95
AF015416

F-NT2RP3004345

35 Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.
7.2e-12:188:71
U22398

F-NT2RP3004355

40 HS_3212_A1_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
Plate=3212 Col=15 Row=E, genomic survey sequence.
0.061:266:65
AQ176625

F-NT2RP3004374

45 HS-1053-B2-E09-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775
Col=18 Row=J, genomic survey sequence.
1.3e-06:181:67
B41504

F-NT2RP3004406

50 CIT-HSP-2340N18.TF CIT-HSP Homo sapiens genomic clone 2340N18, genomic survey sequence.
9.9e-74:359:99
AQ058326

F-NT2RP3004481

55 Mus musculus bassoon gene, exon 6 to 11.
0.0060:528:59

Y17038

F-NT2RP3004552

Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.

7.6e-40:731:64

D64009

F-NT2RP3004557

Human Ki nuclear autoantigen mRNA, complete cds.

8.1e-120:626:94

U11292

F-NT2RP3004625

Homo sapiens I-1 receptor candidate protein mRNA, complete cds.

9.8e-151:710:98

AF082516

F-NT2RP3004640

Bos taurus tuftelin mRNA, complete cds.

8.2e-104:565:87

AF105228

F-NT2RP3004647

Homo sapiens mRNA for KIAA0446 protein, complete cds.

2.1e-109:524:98

AB007915

F-NT2RP4000108

Human gene for neurofilament subunit NF-L.

7.0e-158:862:93

X05608

F-NT2RP4000634

Sequence 11 from patent US 5753446.

2.9e-155:828:92

AR008281

F-NT2RP4000962

Mus musculus clone OST66, genomic survey sequence.

6.0e-48:352:81

AF046696

F-NT2RP4001001

Homo sapiens chromosome 5, Bac clone 58g14 (LBNL H76), complete sequence.

4.8e-47:360:84

AC005915

F-NT2RP4001009

Homo sapiens CAAX prenyl protease (STE24) mRNA, complete cds.

5.9e-175:828:98

AF064867

F-NT2RP4001467

Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).

3.3e-159:742:98

X55740

F-NT2RP4001877

1.7e-27:401:69
AC005637

F-NT2RP4001879

5

F-NT2RP4002187

Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.

4.2e-115:777:83

AF064635

10

F-NT2RP4002451

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111B22, WORKING DRAFT SEQUENCE.

6.1e-86:452:96

Z98200

15

F-NT2RP4002715

Homo sapiens clone NH0523H20, complete sequence.

3.6e-59:410:77

AC005041

20

F-NT2RP4002750

Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds.

3.4e-105:586:87

U70859

25

F-OVARC1000003

B.taurus mRNA for sodium dependent phosphate transporter.

9.0e-125:823:83

X81699

30

F-OVARC1000090

RPCI11-25E14.TP RPCI-11 Homo sapiens genomic clone RPCI-11-25E14, genomic survey sequence.

1.9e-06:151:74

B86784

35

F-OVARC1000105

S.cerevisiae UBC6 gene.

4.6e-25:525:64

X73234

40

F-OVARC1000137

Human SNARE protein Ykt6 (YKT6) mRNA, complete cds.

1.2e-33:184:98

U95735

45

F-OVARC1000208

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-761H5, complete sequence.

1.7e-79:362:91

AC002544

50

F-OVARC1000255

Porcine protein-tyrosine kinase (syk) mRNA, complete cds.

4.9e-116:424:88

M73237

55

F-OVARC1000275

Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.

0.32:314:61
AJ011930

5 F-OVARC1000298
Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.
2.5e-121:306:98
AC005632

10 F-OVARC1000307
Bovine herpesvirus type 1 genes for UL[27,28,29,30,31].
0.017:162:67
X94677

15 F-OVARC1000313
Homo sapiens mRNA for KIAA0573 protein, partial cds.
1.7e-119:585:97
AB011145

20 F-OVARC1000331
Sequence 2 from patent US 5756332.
1.9e-48:290:91
AR009648

25 F-OVARC1000410
Homo sapiens mRNA for angiopoietin-like factor.
4.6e-26:538:62
Y16132

30 F-OVARC1000439
F-OVARC1000467
HS_3008_A2_D12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
Plate=3008 Col=24 Row=G, genomic survey sequence.
2.0e-11:132:82
35 AQ116995

F-OVARC1000529
HS_3092_B2_C11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092
Col=22 Row=F, genomic survey sequence.
40 8.2e-12:115:84
AQ127947

F-OVARC1000553
Homo sapiens chromosome 19, cosmid R26894, complete sequence.
45 6.5e-92:221:96
AC005594

F-OVARC1000775
Human chromosome 3p21.1 gene sequence.
50 6.9e-69:380:95
L13435

F-OVARC1000811
Homo sapiens chromosome 16, cosmid clone 432A1 (LANL), complete sequence.
55 6.7e-77:500:86
AC004235

F-OVARC1000853

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HS_3234_A1_F05_MRCIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3234
Col=9 Row=K, genomic survey sequence.
4.6e-05:111:71
AQ191345

5

F-OVARC1000873
Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene similar to GLU-
COSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence.
8.2e-42:234:96
AL034418

10

F-OVARC1000916
Sequence 3 from patent US 5674748.
2.0e-55:422:84
I68139

15

F-OVARC1000956
Human DNA sequence from cosmid L241B9, Huntington's Disease Region, chromosome 4p16.3 contains poly-
morphic VNTR pYNZ32.
1.2e-107:540:97
Z69708

20

F-OVARC1000995
H.sapiens genomic DNA (chromosome 3; clone NL1106D).
4.3e-28:166:95
X87478

25

F-OVARC1001030
Human mRNA for KIAA0339 gene, complete cds.
2.1e-10:334:64
AB002337

30

F-OVARC1001049
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0190L06; HTGS phase 1,
WORKING DRAFT SEQUENCE, 21 unordered pieces.
5.4e-12:420:62
AC004670

35

F-OVARC1001086
Homo sapiens cyclin T2a mRNA, complete cds.
1.9e-164:761:99
AF048731

40

F-OVARC1001132
Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.
1.5e-89:328:75
AP000038

45

F-OVARC1001163
Caenorhabditis elegans cosmid F40E10, complete sequence.
3.8e-26:337:71
Z69792

50

F-OVARC1001222
CIT-HSP-2010I15.TR CIT-HSP Homo sapiens genomic clone 2010I15, genomic survey sequence.
1.2e-08:171:70
B57734

55

- F-OVARC1001260
- F-OVARC1001336
B.taurus mRNA for sodium dependent phosphate transporter.
5 5.4e-83:622:80
X81699
- F-OVARC1001338
10 HS_2181_B2_E11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2181
Col=22 Row=J, genomic survey sequence.
2.3e-17:144:86
AQ022764
- F-OVARC1001569
15 Mus musculus bone morphogenetic factor 11 (Bmp11) gene, exon 1.
2.9e-06:241:63
AF100904
- F-OVARC1001570
20 Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE.
1.6e-10:235:64
AJ011929
- F-OVARC1001596
25 Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.
2.2e-45:498:73
AC005951
- F-OVARC1001607
30 Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.
1.7e-38:323:80
U15128
- F-OVARC1001725
35 Homo sapiens patched related protein TRC8 (TRC8) gene, exon 1 and partial cds.
3.5e-172:821:98
AF064800
- F-OVARC1001727
40 Human DNA sequence from clone 48A11 on chromosome 20p12 Contains EST, STS, GSS, complete sequence.
2.2e-132:633:98
AL031132
- F-OVARC1001807
45 Human TR3 orphan receptor mRNA, complete cds.
7.1e-90:566:87
L13740
- F-OVARC 1001833
50 Rattus norvegicus cis-Golgi matrix protein GM130 mRNA, complete cds.
5.2e-46:364:79
U35022
- F-OVARC1001952
55 Homo sapiens FGFR-4 gene.
1.7e-14:392:62
Y13901

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5 F-OVARC1001991
Human Chromosome 11 Cosmid cSRL34e5, complete sequence.
2.3e-06:298:64
U73643

10 F-OVARC1002058
, complete sequence.
1.3e-108:617:92
AC005500

15 F-OVARC1002178
Herpes simplex virus type 2 (strain HG52), complete genome.
0.43:234:63
Z86099

20 F-PLACE1000033
Mus musculus otogelin mRNA, complete cds.
5.9e-18:579:59
U96411

25 F-PLACE1000231
Rattus norvegicus WAP four-disulfide core domain protein (ps20) mRNA, complete cds.
1.1e-18:273:68
AF037272

30 F-PLACE1000258
Human KRAB zinc finger protein (ZNP177) mRNA, complete cds.
1.2e-13:241:70
U37263

35 F-PLACE1000442
Human zinc finger protein ZNF136.
2.3e-87:774:76
U09367

40 F-PLACE1000560
Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.
4.1e-107:318:96
AC005368

45 F-PLACE1000740
Rat notch 2 mRNA.
1.1e-37:399:74
M93661

50 F-PLACE1000907
RPC111-73M20.TJ RPC111 Homo sapiens genomic clone R-73M20, genomic survey sequence.
3.5e-21:147:92
AQ269030

55 F-PLACE1000912
F-PLACE1000914
Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.
1.8e-74:206:93
AC002093

F-PLACE1000927

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Cowpox virus strain GRI-90 DNA (49 kb fragment).
6.8e-75:683:74
Y15035

- 5 F-PLACE1000986
RPCI11-75H23.TK RPCI11 Homo sapiens genomic clone R-75H23, genomic survey sequence.
1.0:316:57
AQ268409
- 10 F-PLACE1001016
Human dihydropyridine-sensitive L-type calcium channel alpha-1 subunit (CACNL1A3) mRNA, complete cds.
0.28:432:59
L33798
- 15 F-PLACE1001100
RPCI11-32N5.TK RPCI-11 Homo sapiens genomic clone RPCI-11-32N5, genomic survey sequence.
0.48:145:64
AQ047336
- 20 F-PLACE1001114
Lysobacter enzymogenes beta-lactamase gene sequence.
0.033:349:60
M97392
- 25 F-PLACE1001123
F.rubripes GSS sequence, clone 084A20aC12, genomic survey sequence.
9.7e-05:138:64
AL015804
- 30 F-PLACE1001183
Homo sapiens BAC clone RG318C11 from 7p14-p15, complete sequence.
0.15:576:59
AC005091
- 35 F-PLACE1001229
F.rubripes GSS sequence, clone 144D13aC10, genomic survey sequence.
2.2e-21:271:70
AL017986
- 40 F-PLACE1001231
Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete cds.
6.4e-102:677:84
AF026554
- 45 F-PLACE1001340
Homo sapiens mRNA for KIAA0719 protein, complete cds.
1.3e-130:636:97
AB018262
- 50 F-PLACE1001401
CIT-HSP-2323H22.TR CIT-HSP Homo sapiens genomic clone 2323H22, genomic survey sequence.
6.4e-13:165:76
AQ028562
- 55 F-PLACE1001407
Human DNA sequence from clone 496H19 on chromosome 6q24 Contains ESTs, complete sequence.
2.4e-28:228:85
AL023582

- 5 F-PLACE1001464
Human placental cDNA coding for 5 nucleotidase (EC 3.1.3.5).
5.0e-151:742:96
X55740
- 10 F-PLACE1001500
CIT-HSP-2368L16.TR CIT-HSP Homo sapiens genomic clone 2368L16, genomic survey sequence.
1.1e-25:150:97
AQ078655
- 15 F-PLACE1001516
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.
1.2e-139:676:98
AC002425
- 20 F-PLACE1001536
Human Chromosome X clone bWXD173, WORKING DRAFT SEQUENCE, 2 ordered pieces.
1.7e-142:513:97
AC004387
- 25 F-PLACE1001564
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 287G14, WORKING DRAFT SE-
QUENCE.
2.9e-104:373:89
AL033377
- 30 F-PLACE1001655
Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA, complete cds.
1.3e-123:585:98
AF043472
- 35 F-PLACE1001788
Homo sapiens mRNA for HYA22, complete cds.
9.9e-21:234:75
D88153
- 40 F-PLACE1001795
Drosophila melanogaster; Chromosome 3L; Region 83F1-83F2; P1 clone DS07437, WORKING DRAFT SE-
QUENCE, 3 unordered pieces.
1.4e-05:218:64
AC005985
- 45 F-PLACE1001836
Homo sapiens BAC clone GS155M11 from 7q21-q22, complete sequence.
4.9e-79:577:82
AC004022
- 50 F-PLACE1001918
Arabidopsis thaliana BAC T19D16 genomic sequence.
3.7e-24:417:63
U95973
- 55 F-PLACE1001949
S.cerevisiae chromosome XV reading frame ORF YOR291w.
3.6e-16:255:70
Z75199
- F-PLACE1002080

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Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.
7.5e-129:622:98
AF039691

5 F-PLACE1002095
Homo sapiens chromosome 5, P1 clone 1130f1 (LBNL H40), complete sequence.
2.3e-48:551:71
AC004219

10 F-PLACE1002153
Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.
8.3e-161:764:98
AF095791

15 F-PLACE1002329
Sequence 12 from Patent WO 9000403.
6.9e-05:380:63
I09634

20 F-PLACE1002355
Homo sapiens protease-activated receptor 4 mRNA, complete cds.
2.8e-17:190:77
AF055917

25 F-PLACE1002374
Human mRNA for pro-cathepsin L(major excreted protein MEP).
6.2e-162:716:94
X12451

30 F-PLACE 1002518
HS_3091_A1_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3091
Col=15 Row=K, genomic survey sequence.
3.2e-74:316:94
AQ123005

35 F-PLACE1002547
Homo sapiens mRNA for KIAA0719 protein, complete cds.
2.6e-171:819:98
AB018262

40 F-PLACE1002726
CIT-HSP-2369G10.TR CIT-HSP Homo sapiens genomic clone 2369G10, genomic survey sequence.
4.8e-18:135:88
AQ075115

45 F-PLACE1002905
Drosophila melanogaster DNA sequence (P1 DS00906 (D99)), complete sequence.
3.7e-06:235:66
AC004154

50 F-PLACE1002911
Bovine herpesvirus 1 complete genome.
0.93:264:63
AJ004801

55 F-PLACE1002967
Homo sapiens IgE receptor beta chain (HTm4) mRNA, complete cds.
0.0041:302:60

L35848

F-PLACE1003135

Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.

4.7e-49:450:75

AF024636

F-PLACE1003163

Homo sapiens DBI-related protein mRNA, complete cds.

4.7e-152:722:98

AF069301

F-PLACE1003407

Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds.

6.3e-141:682:97

AF068227

F-PLACE1003428

Human DNA sequence from clone 55C23 on chromosome 6q22.3-23.3 contains vanin-like genes VNN1 and VNN2, ESTs, GSSs,, complete sequence.

1.2e-116:286:100

AL032821

F-PLACE1003438

Pseudomonas alcaligenes outer membrane Xcp-secretion system gene cluster.

0.13:468:60

AF092918

F-PLACE1003460

HS_3234_A1_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3234 Col=9 Row=K, genomic survey sequence.

5.8e-05:111:71

AQ191345

F-PLACE1003529

Homo sapiens clone DJ0981O07, complete sequence.

5.8e-134:457:97

AC006017

F-PLACE1003573

Sequence 2 from patent US 5792648.

0.93:186:62

AR022348

F-PLACE1003598

Mus musculus mismatch repair protein (MSH6) gene, exon 1.

3.3e-07:311:63

AF031085

F-PLACE1003644

Homo sapiens Chromosome 11q23 PAC clone pDJ149k2 containing PLZF gene encoding kruppel-like zinc finger protein, complete sequence.

1.8e-06:138:74

AC001234

F-PLACE1003737

Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete sequence.

1.4e-165:791:98

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- AC005859
- F-PLACE1003772
Human p300/CBP-associated factor (P/CAF) mRNA, complete cds.
5 2.2e-07:448:61
U57317
- F-PLACE1003839
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.
10 2.0e-106:525:97
AC004131
- F-PLACE1003845
Caenorhabditis elegans cosmid D2096.
15 9.8e-26:386:69
U40800
- F-PLACE1003852
Homo sapiens mRNA for KIAA0758 protein, partial cds.
20 7.4e-171:814:98
AB018301
- F-PLACE1004028
- F-PLACE1004078
Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.
25 2.0e-116:274:98
AC005281
- F-PLACE1004166
HS_3223_A1_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223
Col=17 Row=O, genomic survey sequence.
30 0.77:304:58
AQ193346
- F-PLACE1004168
35
- F-PLACE1004199
CIT-HSP-2328F14.TR CIT-HSP Homo sapiens genomic clone 2328F14, genomic survey sequence.
40 9.4e-16:186:76
AQ042262
- F-PLACE1004279
Homo sapiens putative renal organic anion transporter 1 (hROAT1) mRNA, complete cds.
45 1.2e-18:456:62
AF057039
- F-PLACE1004282
- F-PLACE1004305
Homo sapiens mRNA for KIAA0740 protein, complete cds.
50 2.7e-121:612:96
AB018283
- F-PLACE1004441
Human G protein-coupled receptor (GPR1) gene, complete cds.
55 2.4e-104:537:95
U13666

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- 5 F-PLACE1004450
Pleuronectes americanus aminopeptidase N (ampN) mRNA, complete cds.
3.1e-20:601:60
AF012465
- 10 F-PLACE1004482
HS_3032_B1_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
Plate=3032 Col=5 Row=F, genomic survey sequence.
1.1e-86:423:98
AQ129106
- 15 F-PLACE1004492
Human DNA sequence from PAC 434P1 on chromosome 22. Contains inward rectifier potassium channel 4, (po-
tassium channel, inwardly rectifying, subfamily J, member 4) (hippocampal inward rectifier) (HIR) (HRK1) (HIRK2)
(KIR2.3), ESTs similar to lumen protein retaining receptor 2 (KDEL receptor 2), DEAD-box protein P72, ESTs, CpG
islands.
0.17:180:67
Z97056
- 20 F-PLACE1004519
Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene,
VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete
sequence.
1.1e-75:432:84
25 AL021808
- F-PLACE1004520
Human pregnancy-specific beta-1-glycoprotein mRNA PSG95, complete cds.
4.1e-109:606:92
30 M34715
- F-PLACE1004630
Homo sapiens mRNA for osteoblast specific cysteine-rich protein, complete cds.
6.2e-138:749:92
35 AB008375
- F-PLACE1004637
HS-1061-B1-E10-MFabi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 783
Col=19 Row=J, genomic survey sequence.
0.013:92:75
40 B45487
- F-PLACE1004648
- 45 F-PLACE1004816
Homo sapiens mRNA for Hakata antigen, complete cds.
3.8e-98:590:90
D88587
- 50 F-PLACE1004887
Dog alpha-L-iduronidase (IDUA) gene, exons 7-12.
1.2e-06:469:60
L01060
- 55 F-PLACE1005003
Human SNC19 mRNA sequence.
4.8e-20:472:63
U20428

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- F-PLACE1005005
Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.
7.8e-143:650:97
5 AJ011930
- F-PLACE1005031
Bovine chloride channel protein (p64) mRNA, complete cds.
7.1e-62:463:83
10 L16547
- F-PLACE1005239
Homo sapiens mRNA for HIRIP3 protein, clone pH4-31.
2.2e-14:115:85
15 AJ223349
- F-PLACE1005250
Mus musculus maternal transcript Maid (Maid) mRNA, complete cds.
3.3e-40:370:77
20 U50734
- F-PLACE1005383
Homo sapiens UP50 mRNA, complete cds.
2.7e-126:633:96
25 AF093118
- F-PLACE1005410
Rattus rattus sec61 homologue mRNA, complete cds.
1.9e-115:771:85
30 M96630
- F-PLACE1005426
Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence.
7.2e-113:391:96
35 AC005392
- F-PLACE1005519
Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.
1.0e-53:521:74
40 AF024636
- F-PLACE1005539
c-erbB=proto-oncogene {exon 1, promoter} [chickens, Genomic, 700 nt].
3.6e-05:434:62
45 S66408
- F-PLACE1005544
Mus musculus junctional adhesion molecule (Jam) mRNA, complete cds.
3.3e-56:575:74
50 U89915
- F-PLACE1005569
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.
1.1e-118:381:96
55 AL034397
- F-PLACE1005601
Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.

3.9e-143:697:98
AC002073

F-PLACE1005660

5

F-PLACE1005669

Fruit fly (*D.melanogaster*) Glued mRNA, complete cds.

3.4e-14:275:66

J02932

10

F-PLACE1005682

Mus musculus Ankhzn mRNA, complete cds.

0.75:347:57

AB011370

15

F-PLACE1005725

Homo sapiens huntingtin (HD) gene, exon 1.

1.4e-06:425:62

L27350

20

F-PLACE1005736

F-PLACE1005745

HS_3039_B1_F12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039

25

Col=23 Row=L, genomic survey sequence.

1.0:283:59

AQ155068

F-PLACE1005768

30

Human DNA sequence from Fosmid 24E5 on chromosome 22q11.2-qter contains parvalbumin, ESTs, STS.

1.5e-141:719:96

Z82185

F-PLACE1005815

35

Sequence 1 from patent US 5571905.

0.088:199:62

I28535

F-PLACE1005878

40

Bovine chlorine channel protein (p64) mRNA, complete cds.

2.5e-54:394:84

L16547

F-PLACE1005927

45

HS_3138_B2_B03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3138

Col=6 Row=D, genomic survey sequence.

8.0e-32:162:95

AQ183333

F-PLACE1006071

50

1.6e-180:877:96

AF028816

F-PLACE1006073

55

Homo sapiens mRNA for glucuronyltransferase I, complete cds.

1.7e-94:464:98

AB009598

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5 F-PLACE1006079
Homo sapiens distal-less homeobox protein (DLX3) gene, complete cds.
5.2e-107:423:96
AF028233

10 F-PLACE1006093
jd187 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 5H9, genomic survey se-
quence.
0.00018:316:60
B13419

15 F-PLACE1006208
Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.
1.4e-12:421:64
L14320

20 F-PLACE1006219
Caenorhabditis elegans cosmid D2096.
6.4e-25:386:69
U40800

25 F-PLACE1006277
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.
7.2e-135:381:97
AL034397

30 F-PLACE1006290
Caenorhabditis elegans cosmid F09E5.
1.4e-08:354:61
U37429

35 F-PLACE1006443
Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.
2.9e-80:168:95
AC002093

40 F-PLACE1006515
Homo sapiens mRNA for KIAA0576 protein, partial cds.
4.2e-140:655:99
AB011148

45 F-PLACE1006716
Human DNA sequence from PAC 151B14 on chromosome 22q12-qter contains somatostatin receptor subtype 3
(SSTR3), tRNA, ESTs, CpG island and STS.
2.2e-51:621:70
Z86000

50 F-PLACE1006786
CITBI-E1-2502A9.TR CITBI-E1 Homo sapiens genomic clone 2502A9, genomic survey sequence.
0.43:237:64
AQ264473

55 F-PLACE1006809
HS_2255_B1_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255
Col=9 Row=L, genomic survey sequence.
2.1e-14:95:97
AQ131814

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F-PLACE1006959
 HS_3247_B1_E03_MRCIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3247
 Col=5 Row=J, genomic survey sequence.
 1.1e-09:199:70
 5 AQ220414

F-PLACE1007028
 Homo sapiens Chromsome 11p15.5 PAC clone pDJ754h15 containing cdk-inhibitor p57/KIP2 (CDKN1C) gene,
 complete sequence.
 10 2.0e-24:658:62
 AC005950

F-PLACE1007040
 Mus musculus neuronal intermediate filament protein (alpha-internexin) gene, complete cds.
 15 8.8e-09:585:62
 L27220

F-PLACE1007077

20 F-PLACE1007081
 RPCI11-31D7.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-31D7, genomic survey sequence.
 2.3e-42:228:97
 AQ016433

25 F-PLACE1007096

F-PLACE1007296
 Human mRNA for a presumptive KDEL receptor.
 1.3e-71:542:83
 30 X55885

F-PLACE1007591
 Homo sapiens full length insert cDNA clone YP44A02.
 1.1e-18:141:90
 35 AF085890

F-PLACE1007626
 Homo sapiens unknown mRNA, complete cds.
 7.8e-104:516:97
 40 AF047439

F-PLACE1007702
 Homo sapiens chromosome 17, clone 363G12, WORKING DRAFT SEQUENCE, 11 unordered pieces.
 7.5e-50:439:77
 45 AC002348

F-PLACE1007845
 Caenorhabditis elegans cosmid F09E5.
 4.4e-08:355:62
 50 U37429

F-PLACE1007881
 CITBI-E1-2517N6.TF CITBI-E1 Homo sapiens genomic clone 2517N6, genomic survey sequence.
 1.4e-14:104:95
 55 AQ279407

F-PLACE1007971
 HS_3237_B2_F09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3237

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Col=18 Row=L, genomic survey sequence.

1.2e-12:169:76

AQ206052

5

F-PLACE1008282

Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.

4.5e-101:192:100

AC005995

10

F-PLACE1008297

Mycoplasma genitalium random genomic clone hg1, partial cds.

0.099:193:60

U02109

15

F-PLACE1008359

Homo sapiens DNA for (CGG)_n trinucleotide repeat region, isolate CL16-1 (Chr.16).

0.53:185:65

AJ001218

20

F-PLACE1008469

Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.

1.2e-93:213:98

AC002093

25

F-PLACE1008549

Homo sapiens E74-like factor 5 (ELF5) mRNA, complete cds.

5.7e-144:693:98

AF049703

30

F-PLACE1008657

Bovine mRNA for adseverin, complete cds.

5.6e-140:782:90

D26549

35

F-PLACE1008716

Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.

1.1e-133:648:97

U15128

40

F-PLACE1008744

Sequence 1 from patent US 5691147.

8.4e-91:475:95

I76197

45

F-PLACE1008984

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SE-
QUENCE.

4.2e-103:493:99

AL031427

50

F-PLACE1008985

Mus musculus synaptotagmin VIII mRNA, partial cds.

1.1e-23:289:72

U20107

55

F-PLACE1009067

H.sapiens CpG island DNA genomic MseI fragment, clone 52e12, forward read cpg52e12.ft1a.

1.2e-28:164:96

- Z61442
- F-PLACE1009196
- 5 F-PLACE1009279
H.sapiens mRNA for serine protease.
6.0e-10:327:64
Y07921
- 10 F-PLACE1009527
Human DNA-binding protein ABP/ZF mRNA, complete cds.
2.0e-19:125:96
U82613
- 15 F-PLACE1009546
S.lividans mercury resistance operon.
0.56:358:59
X65467
- 20 F-PLACE1009600
Mouse mRNA for tetracycline transporter-like protein, complete cds.
2.1e-128:718:91
D88315
- 25 F-PLACE1009735
Homo sapiens clone NH0523H20, complete sequence.
2.9e-128:613:99
AC005041
- 30 F-PLACE1009982
- F-PLACE1010011
, complete sequence.
2.1e-26:234:83
35 AC005409
- F-PLACE1010078
Saccharomyces cerevisiae chromosome XII cosmid 8300.
0.066:273:58
40 U19028
- F-PLACE1010081
Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.
7.0e-150:733:97
45 AF027706
- F-PLACE1010251
Sequence 1 from patent US 5665588.
0.0012:309:62
50 I64695
- F-PLACE1010445
Herpes simplex virus type 2 (strain HG52), complete genome.
9.4e-07:511:58
55 Z86099
- F-PLACE1010713
Mus musculus putative steroid dehydrogenase (KIK-I) mRNA, complete cds.

- 2.1e-89:612:83
AF064635
- 5 F-PLACE1010784
Sequence 1 from patent US 5686597.
2.5e-103:505:98
I73723
- 10 F-PLACE1010827
Cricetulus griseus COP-coated vesicle membrane protein CHOp24 mRNA, partial cds.
7.3e-13:327:66
U26264
- 15 F-PLACE1010968
O.cuniculus mRNA for titin.
0.44:165:64
X64696
- 20 F-PLACE1011045
Homo sapiens E1-like protein mRNA, complete cds.
1.8e-127:595:99
AF094516
- 25 F-PLACE1011116
HS_2033_A2_E05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033
Col=10 Row=I, genomic survey sequence.
8.3e-29:192:92
AQ229784
- 30 F-PLACE1011181
H.sapiens CpG island DNA genomic Mse1 fragment, clone 99f2, reverse read cpg99f2.rt1a.
4.8e-35:200:95
Z64239
- 35 F-PLACE1011236
Mus musculus mRNA for RST, complete cds.
4.5e-54:717:66
AB005451
- 40 F-PLACE1011364
Homo sapiens protein kinase/endoribonulcease (IRE1) mRNA, complete cds.
0.13:502:57
AF059198
- 45 F-PLACE1011407
M.domesticus (C57B1/6J) mRNA for zinc finger protein 30.
7.2e-15:313:68
Z30174
- 50 F-PLACE1011516
Drosophila melanogaster; Chromosome 3L; Region 79F1-80A2; BAC clone BACR48E05, WORKING DRAFT SE-
QUENCE, 4 unordered pieces.
1.8e-16:317:66
AC005720
- 55 F-PLACE1011708
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.
1.8e-143:722:96

AF034611

F-PLACE1011824

Human Ste20-like kinase (MST2) mRNA, complete cds.

5.0e-100:561:92

U26424

F-PLACE 101 1978

Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.

9.6e-76:722:74

M27877

F-PLACE2000118

Homo sapiens DNA sequence from PAC 393P12 on chromosome Xp11.21. Contains a hypothetical protein KIAA0413 (KIAA0412, KIAA0065, KIAA0569) LIKE Zinc Finger protein pseudogene, a hypothetical Proline-rich protein KIAA0269 LIKE gene and a 60S Ribosomal Protein L7 LIKE pseudogene. Contains ESTs, an STS and a GSS (BAC end sequence), complete sequence.

5.2e-112:568:95

AL022578

F-PLACE2000219

Homo sapiens Down Syndrome critical region, partial sequence.

0.0059:144:71

AF015262

F-PLACE3000181

Sequence 102 from patent US 5643781.

4.1e-127:745:90

I51041

F-PLACE3000213

F-PLACE4000354

HS_3071_A2_B06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071

Col=12 Row=C, genomic survey sequence.

4.4e-12:335:64

AQ137396

F-PLACE4000455

Homo sapiens transcriptional enhancer factor (TEF1) DNA, complete CDS.

9.5e-118:563:98

M63896

F-SKNMC1000004

Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.

2.9e-141:292:98

AC005632

F-SKNMC1000014

CIT-HSP-2359K11.TR CIT-HSP Homo sapiens genomic clone 2359K11, genomic survey sequence.

0.89:136:67

AQ075724

F-SKNMC1000082

H.sapiens CpG island DNA genomic MseI fragment, clone 26g3, reverse read cpg26g3.rt1b.

5.6e-06:60:98

265216

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- F-THYRO1000036
- F-THYRO1000061
Homo sapiens chromosome 19, cosmid R28991, complete sequence.
5 2.4e-105:425:94
AC004623
- F-THYRO1000099
Rattus norvegicus leukocyte common antigen receptor (LAR) gene, trans-spliced alternative untranslated exon.
10 0.35:609:57
U87960
- F-THYRO1000196
Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds.
15 5.1e-125:475:98
AF016272
- F-THYRO1000400
Mycobacterium tuberculosis sequence from clone y423.
20 1.0:264:59
AD000014
- F-THYRO1000580
HS_3216_A1_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3216
25 Col=17 Row=O, genomic survey sequence.
2.8e-25:157:96
AQ184086
- F-THYRO1000584
Boar mRNA for 135kDa protein, complete cds.
30 2.0e-104:787:80
D28521
- F-THYRO1000678
M.musculus Cx30 gene.
35 6.9e-41:285:85
Z70023
- F-THYRO1000776
Drosophila melanogaster DNA sequence (P1 DS08948 (D168)), complete sequence.
40 2.7e-10:389:59
AC004288
- F-THYRO1000795
Rattus norvegicus mRNA for mitochondrial dicarboxylate carrier.
45 1.2e-107:736:83
AJ223355
- F-THYRO1000846
CITBI-E1-2505H6.TR CITBI-E1 Homo sapiens genomic clone 2505H6, genomic survey sequence.
50 0.00025:351:61
AQ260270
- F-THYRO1000866
Homo sapiens SKB1Hs mRNA, complete cds.
55 3.3e-91:529:89
AF015913

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- 5 F-THYRO1000956
Human G protein-coupled receptor APJ gene, complete cds.
3.8e-148:724:97
U03642
- 10 F-THYRO1000964
Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.
5.0e-37:714:64
AF091624
- 15 F-THYRO1000999
CITBI-E1-2508B3.TF CITBI-E1 Homo sapiens genomic clone 2508B3, genomic survey sequence.
1.2e-06:280:62
AQ261426
- 20 F-THYRO1001063
H.sapiens (xs174) mRNA, 300bp.
1.6e-41:298:85
Z36825
- 25 F-THYRO1001071
Human mRNA for KIAA0154 gene, partial cds.
7.4e-16:197:73
D63876
- 30 F-THYRO1001102
Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.
3.5e-10:128:83
AC004997
- 35 F-THYRO1001113
Homo sapiens mRNA for LGMD2B protein.
8.8e-52:684:68
AJ007670
- 40 F-THYRO1001128
Homo sapiens chromosome 9q34, clone 63G10, complete sequence.
1.2e-141:227:97
AC002096
- 45 F-THYRO1001205
F-THYRO1001237
Mus musculus interleukin-2 (Il-2) gene, 5'end.
0.77:78:74
L07576
- 50 F-THYRO1001242
Mouse mRNA for thymic epithelial cell surface antigen, complete cds.
5.1e-127:721:90
D67067
- 55 F-THYRO1001266
Human sodium iodide symporter mRNA, complete cds.
2.7e-41:806:62
U66088
- F-THYRO1001327

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Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.

3.1e-117:374:96

AL021578

F-THYRO1001456

F-THYRO1001457

M.musculus (Balb/c) mRNA for serine/threonine protein kinase.

1.8e-57:491:69

Z34524

F-THYRO1001471

Sequence 52 from Patent WO9712992.

0.00019:546:58

A62364

F-THYRO1001478

F-THYRO1001495

Homo sapiens clone DJ1163L11, complete sequence.

4.4e-20:222:76

AC005230

F-THYRO1001523

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 407F17, WORKING DRAFT SEQUENCE.

8.8e-21:538:62

Z83845

F-THYRO1001529

M.musculus mRNA for serine palmitoyltransferase subunit B.

5.8e-32:448:66

X95642

F-THYRO1001593

Homo sapiens chromosome 19, cosmid R31237, complete sequence.

5.8e-91:213:98

AC005581

F-THYRO1001608

Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.

0.0028:335:65

AE000662

F-THYRO1001641

Leishmania major chromosome 3 clone L6290 strain Friedlin, WORKING DRAFT SEQUENCE, 2 ordered pieces.

0.92:378:61

AC005928

F-THYRO1001700

HS_3220_A1_B08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=15 Row=C, genomic survey sequence.

1.0e-49:265:96

AQ184388

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- 5 F-THYRO1001702
Mus musculus mRNA for myeloid associated differentiation protein.
1.4e-70:502:82
AJ001616
- 10 F-THYRO1001725
F.rubripes GSS sequence, clone 133B16aE1, genomic survey sequence.
3.8e-06:249:65
AL004967
- 15 F-THYRO1001770
S.cerevisiae chromosome II reading frame ORF YBR059c.
1.5e-07:320:62
Z35928
- 20 F-THYRO1001803
Homo sapiens chromosome 10 clone CRI-JC2019 map 10q22.1-10q22.2, WORKING DRAFT SEQUENCE, 1
ordered pieces.
1.2e-38:234:94
AC006108
- 25 F-Y79AA1000030
Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.
9.9e-92:389:98
AC005214
- 30 F-Y79AA1000127
Homo sapiens genomic DNA, chromosome 21q11.1, segment 5/28, WORKING DRAFT SEQUENCE.
9.2e-131:359:100
AP000034
- 35 F-Y79AA1000207
Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.
2.2e-151:302:98
AC005562
- 40 F-Y79AA1000226
Drosophila melanogaster, chromosome 2L, region 21C5-21D1, P1 clone DS07610, complete sequence.
1.1e-50:549:67
AC004573
- 45 F-Y79AA1000270
Bos taurus vacuolar H+ ATPase subunit Ac45 mRNA, complete cds.
6.4e-111:771:83
U10039
- 50 F-Y79AA1000426
Mus musculus activin beta E subunit mRNA, complete cds.
2.4e-87:703:76
U96386
- 55 F-Y79AA1000521
Homo sapiens LERK-6 (EPLG6) gene, exon 1.
0.0092:148:68
U92893
- F-Y79AA1000750
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-761H5, complete sequence.

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9.0e-07:143:74
AC002544

F-Y79AA1000776

5

F-Y79AA1000777

Podospira anserina beta transducin-like protein (het-e1) gene, complete cds.

6.6e-17:760:59
L28125

10

F-Y79AA1000876

Homo sapiens long form transcription factor C-MAF (c-maf) mRNA, complete cds.

3.3e-10:323:66
AF055377

15

F-Y79AA1000888

Streptomyces coelicolor cosmid 8A6.

3.1e-06:665:59
AL031013

20

F-Y79AA1000959

Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds.

1.6e-52:277:96
AF093420

25

F-Y79AA1000967

Rattus norvegicus vesicle-associate calmodulin-binding protein mRNA, complete cds.

2.9e-131:752:86
L22557

30

F-Y79AA1001013

F-Y79AA1001056

Mus musculus maternal transcript Maid (Maid) mRNA, complete cds.

35

1.2e-85:676:79
U50734

F-Y79AA1001062

Human Chromosome 11 Cosmid cSRL34e5, complete sequence.

40

8.6e-17:293:65
U73643

F-Y79AA1001090

Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.

45

1.9e-05:223:63
AC004596

F-Y79AA1001212

Homo sapiens SL15 protein mRNA, complete cds.

50

4.7e-162:763:98
AF038961

F-Y79AA1001264

Drosophila melanogaster DNA sequence (P1s DS00764 (D273) and DS00501 (D274)), complete sequence.

55

1.2e-32:599:63
AC005269

F-Y79AA1001272

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Homo sapiens *** SEQUENCING IN PROGRESS *** from cosmid 5L5, WORKING DRAFT SEQUENCE.

1.2e-11:356:67

AJ009613

5

F-Y79AA1001328

Rattus norvegicus Delta 3 mRNA, complete cds.

2.1e-51:443:76

AF084576

10

F-Y79AA1001426

HS_3146_A1_A10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3146

Col=19 Row=A, genomic survey sequence.

9.0e-23:106:91

AQ141090

15

F-Y79AA1001427

Bovine cytochrome b5 reductase mRNA, partial cds.

1.4e-55:670:70

M83104

20

F-Y79AA1001430

Homo sapiens mRNA for KIAA0469 protein, complete cds.

8.6e-123:577:99

AB007938

25

F-Y79AA1001523

Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds.

3.3e-91:496:93

AF009353

30

F-Y79AA1001530

Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.

1.8e-126:764:89

AL030996

35

F-Y79AA1001592

HS_3219_A2_E12_MRC CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219

Col=24 Row=I, genomic survey sequence.

5.2e-36:234:89

AQ180547

40

F-Y79AA1001727

F-Y79AA1001787

S.pombe chromosome III cosmid c1672.

8.8e-11:409:58

50

AL031324

F-Y79AA1001793

Fugu rubripes GSS sequence, clone 027L23aG3, genomic survey sequence.

0.12:131:70

55

AL025355

F-Y79AA1001795

Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the BINGS gene, exons 11

- to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a pseudogene similar to TAT-SF1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6 (RING2), the gene for HKE4 (RINGS), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen, type XI, alpha 2) gene, the HLA-DPB2 pseudogene and part of the HLA-DPA3 pseudogene. Contains predicted CpG islands, ESTs, STSs, and GSSs, complete sequence.
1.2e-140:672:98
AL031228
- 5
- F-Y79AA1001799
S.pombe chromosome I cosmid c8C9.
0.00031:300:60
Z99168
- 10
- F-Y79AA1001803
Mus musculus secretogranin III (SgIII) mRNA, complete cds.
4.6e-101:516:82
U02982
- 15
- F-Y79AA1001863
Homo sapiens DNA, anonymous heat-stable fragment RP5-6A.
5.2e-85:410:99
AB012170
- 20
- F-Y79AA1002022
CIT-HSP-2053H1.TF CIT-HSP Homo sapiens genomic clone 2053H1, genomic survey sequence.
4.3e-20:130:95
B68526
- 25
- F-Y79AA1002058
Homo sapiens clone 24733 mRNA sequence.
5.3e-153:740:98
AF052149
- 30
- F-Y79AA1002121
F-Y79AA1002129
Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.
5.5e-12:565:61
L14320
- 35
- F-Y79AA1002213
Rattus norvegicus brain specific Na⁺-dependent inorganic phosphate cotransporter mRNA, complete cds.
4.0e-12:434:60
U07609
- 40
- F-Y79AA1002334
F.rubripes GSS sequence, clone 174E24aB10, genomic survey sequence.
3.0e-10:171:72
AL019366
- 45
- F-Y79AA1002373
Rattus norvegicus Smad8 mRNA, complete cds.
0.96:420:61
AF012347
- 50
- F-Y79AA1002376
Rattus norvegicus cytoplasmic dynein intermediate chain 2B mRNA, complete cds.
- 55

1.1e-132:805:88
U39045

5 F-Y79AA1002378
Mus musculus mRNA for zinc finger protein, complete cds, clone:CTfin51.
1.9e-64:521:78
D10630

10 F-Y79AA1002381
O.sativa mRNA for cdc2+/CDC28-related protein kinase.
3.3e-21:431:60
X58194

Homology search result 7

15 [0298] The result of the homology search in the GenBank(<http://www.ncbi.nlm.nih.gov/web/GenBank/>) using the clone sequences of the 3'-ends. except EST and STS sequences.

20 Indicated are from the top,
the name of the clone sequence,
definition of the top hit data,
the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
the Accession No. of the top hit data.

25 [0299] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone. Data were not shown for the clones in which the P-value was higher than 1.

R-HEMBA1000006

30 R-HEMBA1000121
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT SE-
QUENCE.
2.2e-43:355:80
AL031291

35 R-HEMBA1000128
Homo sapiens chromosome X, PAC 671D9, complete sequence.
0.99:389:60
AF031078

40 R-HEMBA1000275
Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG
island.
3.4e-10:212:66
45 Z93023

R-HEMBA1000300
{Alu RNA transcript, clone NE461} [human, embryonal carcinoma cells, NTera2D1 pluripotent cells, Other RNA,
282 nt].
50 4.6e-42:246:89
S42653

R-nnnnnnnnnnnnn
Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence.
55 1.0e-71:192:95
AC005922

R-HEMBA1000462

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Homo sapiens clone 243 unknown mRNA, complete sequence.
8.3e-90:313:94
AF091094

5 R-HEMBA1000477
Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 8/11.
0.22:377:60
AB020865

10 R-HEMBA1000590
Homo sapiens mRNA for matrilin-4, partial.
8.0e-101:547:93
AJ007581

15 R-HEMBA1000634
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0539L10; HTGS phase 1, WORKING DRAFT SEQUENCE, 15 unordered pieces.
0.95:186:62
20 AC004480

R-HEMBA1000671
RPC111-65E1.TJ RPC111 Homo sapiens genomic clone R-65E1, genomic survey sequence.
2.1e-09:165:73
25 AQ237194

R-HEMBA1000713
Homo sapiens 10kD protein (BC10) mRNA, complete cds.
1.2e-117:575:97
30 AF053470

R-HEMBA1000732
Homo sapiens mRNA for latent transforming growth factor-beta binding protein-4.
1.4e-108:581:93
35 Y13622

R-nnnnnnnnnnnnn

40 R-HEMBA1000875
Homo sapiens chromosome 17, clone hRPK.1090_M_7, complete sequence.
0.044:253:64
AC005274

R-HEMBA1000940
45 ***ALU WARNING: Human Alu-J subfamily consensus sequence.
1.9e-33:222:82
U14567

50 R-HEMBA1000962

R-HEMBA1001184
Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.
0.00044:466:58
55 AC004688

R-HEMBA1001221
Sequence 1 from patent US 5633147.

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- 7.1e-11:232:65
I43819
- 5 R-HEMBA1001228
Human germline oligomeric matrix protein (COMP) mRNA, complete cds.
7.8e-89:358:96
L32137
- 10 R-HEMBA1001272
nxb0003bDO1r CUGI Rice BAC Library Oryza sativa genomic clone nxb0003G00r, genomic survey sequence.
0.00014:201:64
AQ050116
- 15 R-HEMBA1001296
Homo sapiens PAC clone DJ1168D11 from 7p21-p22, complete sequence.
0.13:440:58
AC004614
- 20 R-HEMBA1001297
Homo sapiens putative transcription factor CA150 mRNA, complete cds.
5.0e-92:466:96
AF017789
- 25 R-HEMBA1001390
CIT-HSP-2314K10.TR CIT-HSP Homo sapiens genomic clone 2314K10, genomic survey sequence.
3.4e-43:196:85
AQ027191
- 30 R-HEMBA1001563
H.sapiens villin gene, exon 1.
2.1e-43:342:81
X71058
- 35 R-HEMBA1001621
Human G protein-coupled receptor APJ gene, complete cds.
1.2e-41:288:87
U03642
- 40 R-HEMBA1001878
Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds.
2.0e-79:434:93
AF090988
- 45 R-HEMBA1001886
Human zinc finger protein (ZNF141) mRNA, complete cds.
1.8e-59:530:80
L15309
- 50 R-HEMBA1002048
Homo sapiens chromosome 5, P1 clone 1307e8 (LBNL H60), complete sequence.
0.36:322:61
AC005355
- 55 R-HEMBA1002131
Human DNA sequence from clone 301K23 on chromosome 1p35.1-36.21. Contains the 5' part of a novel gene similar to predicted yeast and worm genes. Contains ESTs and GSSs, complete sequence.
0.22:233:61
AL031730

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- 5 R-HEMBA1002163
Homo sapiens chromosome X, clone 592, WORKING DRAFT SEQUENCE, 8 unordered pieces.
1.1e-16:275:69
AC002489
- 10 R-HEMBA1002167
Rattus norvegicus neuroligin I mRNA, complete cds.
8.7e-23:193:84
U22952
- 15 R-HEMBA1002178
- R-HEMBA1002195
Homo sapiens DHPS gene, exons 8 to 9.
1.4e-19:114:100
AJ001704
- 20 R-HEMBA1002227
Homo sapiens mRNA for 80K-L protein, complete cds.
6.1e-115:567:97
D10522
- 25 R-HEMBA1002316
Homo sapiens mRNA for putative GTP-binding protein.
1.5e-18:161:85
Y14391
- 30 R-HEMBA1002420
Caenorhabditis elegans cosmid C27A7, complete sequence.
0.88:214:62
Z81041
- 35 R-HEMBA1002421
Human heparan sulfate proteoglycan (HSPG) core protein, 3' end.
6.0e-90:443:97
J04621
- 40 R-HEMBA1002524
Human MHC Class I region proline rich protein mRNA, complete cds.
3.2e-110:551:96
U63336
- 45 R-HEMBA1002551
Mouse Bac 276o8, WORKING DRAFT SEQUENCE, 25 unordered pieces.
7.0e-06:397:61
AC003022
- 50 R-HEMBA1002767
Homo sapiens clone NH0486122, WORKING DRAFT SEQUENCE, 5 unordered pieces.
4.2e-110:568:96
AC005038
- 55 R-HEMBA1002985
Homo sapiens chromosome 17, clone hRPK.15_K_2, complete sequence.
3.4e-23:184:86
AC005901
- R-HEMBA1003047

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Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.
5.0e-114:571:96
AF034611

5 R-HEMBA1003072
HS-1014-B1-F12-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 789
Col=23 Row=L, genomic survey sequence.
1.5e-62:340:94
B32084

10 R-HEMBA1003101
Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.
3.8e-116:575:97
AF049891

15 R-HEMBA1003120
HS_3220_A1_F04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220
Col=7 Row=K, genomic survey sequence.
3.6e-61:354:92
20 AQ184345

R-HEMBA1003230
Homo sapiens UP50 mRNA, complete cds.
1.3e-42:258:93
25 AF093118

R-HEMBA1003294
HS_3220_A1_D03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220
Col=5 Row=G, genomic survey sequence.
30 0.0095:204:63
AQ190655

R-HEMBA1003315
Sus scrofa DNA for LH beta, exons 1, 2, 3, complete cds.
35 6.6e-24:163:79
D00579

R-HEMBA1003392
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.
40 2.6e-115:557:98
AF074264

R-HEMBA1003399
Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.
45 1.8e-63:166:100
AC004971

R-HEMBA1003487

50 R-HEMBA1003497
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27O5, WORKING DRAFT SEQUENCE.
1.4e-119:592:97
AL033529

55 R-HEMBA1003530

R-HEMBA1003602
Human Chromosome 16 BAC clone CIT987SK-A-17E1, complete sequence.

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- 9.4e-79:468:91
AC002041
- 5 R-HEMBA1003732
Homo sapiens clone DJ0935K16, complete sequence.
2.0e-118:586:98
AC006011
- 10 R-HEMBA1003945
Human calcineurin B mRNA, complete cds.
8.9e-82:410:97
M30773
- 15 R-HEMBA1004007
Homo sapiens clone DJ0665P05, WORKING DRAFT SEQUENCE, 5 unordered pieces.
6.7e-56:404:75
AC004851
- 20 R-HEMBA1004085
G.gallus microsatellite DNA (LEI0311 (= EC12A05)).
0.66:144:65
Z95196
- 25 R-nnnnnnnnnnnnn
Homo sapiens intersectin short form mRNA, complete cds.
2.1e-115:569:97
AF064243
- 30 R-HEMBA1004250
Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H161), complete sequence.
3.8e-98:478:98
AC005752
- 35 R-HEMBA1004391
Plasmodium falciparum MAL3P8, complete sequence.
0.29:126:65
AL034560
- 40 R-HEMBA1004444
Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.
8.4e-52:308:78
AC004938
- 45 R-HEMBA1004454
CIT-HSP-2337122.TF CIT-HSP Homo sapiens genomic clone 2337122, genomic survey sequence.
0.78:59:77
AQ038475
- 50 R-HEMBA1004505
R-HEMBA1004785
R-HEMBA1004797
- 55 R-HEMBA1004952
Mus musculus diabetic embryopathy (Dep-1) mRNA.
3.4e-39:327:82
AF032130

- 5 R-HEMBA1004971
Homo sapiens BAC clone RG351J01 from 7q22-q31, complete sequence.
0.00040:251:66
AC005099
- 10 R-HEMBA1004982
Strongyloides fulleborni 18S ribosomal RNA and 5.8S ribosomal RNA genes, partial sequence, and internal transcribed spacer 1, complete sequence.
0.092:191:63
U43581
- 15 R-HEMBA1005070
Human mRNA for KIAA0310 gene, complete cds.
1.2e-94:381:91
AB002308
- R-HEMBA1005084
- 20 R-HEMBA1005145
Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.
5.7e-58:283:84
AJ003147
- 25 R-HEMBA1005230
CIT-HSP-2333N15.TR CIT-HSP Homo sapiens genomic clone 2333N15, genomic survey sequence.
5.5e-31:363:73
AQ040189
- 30 R-HEMBA1005246
Homo sapiens full length insert cDNA clone YX52E07.
1.6e-11:173:72
AF086040
- 35 R-HEMBA1005267
Sequence 1 from patent US 5618695.
2.4e-73:536:81
I40055
- 40 R-HEMBA1005337
Caenorhabditis elegans cosmid K07D4.
0.16:157:63
AF077534
- 45 R-HEMBA1005430
- R-HEMBA1005449
- 50 R-HEMBA1005489
Anopheles rangeli NADH dehydrogenase subunit 2 gene, mitochondrial gene encoding mitochondrial product, partial cds.
0.020:271:61
U35272
- 55 R-HEMBA1005522
- R-HEMBA1005545
Human m3 muscarinic acetylcholine receptor (CHRM3) gene, complete cds.

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- 1.8e-115:579:96
U29589
- 5 R-HEMBA1005698
0.0065:223:65
AG004952
- 10 R-HEMBA1005913
Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.
3.7e-15:272:68
AC003037
- 15 R-HEMBA1005929
Homo sapiens chromosome 19, cosmid R31237, complete sequence.
9.4e-55:502:76
AC005581
- 20 R-HEMBA1005945
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 774G10, WORKING DRAFT SE-
QUENCE.
0.45:245:62
AL034410
- 25 R-HEMBA1006016
Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.
3.5e-25:415:66
AC005562
- 30 R-HEMBA1006171
Human DNA sequence from PAC 433M19 on chromosome Xq26.3-Xq27.1. Contains ESTs, STSs and polymorphic
CA repeat.
1.0:176:64
Z95703
- 35 R-HEMBA1006276
Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.
2.8e-118:592:96
AC005261
- 40 R-HEMBA1006299
- R-HEMBA1006311
- 45 R-HEMBA1006335
Human DNA sequence from clone 496H19 on chromosome 6q24 Contains ESTs, complete sequence.
6.1e-111:578:96
AL023582
- 50 R-HEMBA1006357
Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.
4.8e-11:174:74
AC004469
- 55 R-HEMBA1006430
Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.
8.7e-45:402:79
AC004086

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R-HEMBA1006482
 Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.
 1.7e-105:537:96
 AF026852

5

R-HEMBA1006517
 345A19.TV CIT978SKA1 Homo sapiens genomic clone A-345A19, genomic survey sequence.
 1.5e-44:176:88
 B15409

10

R-HEMBA1006544
 Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.
 2.5e-66:310:83
 AC004997

15

R-HEMBA1006572
 Homo sapiens reduced folate carrier (RFC1) gene, exons 1a, 1c and 1b.
 0.028:255:64
 U92868

20

R-HEMBA1006658
 Homo sapiens mRNA for KIAA0687 protein, partial cds.
 7.3e-1 11:570:94
 AB014587

25

R-HEMBA1006707
 Homo sapiens mRNA for matrilin-4, partial.
 5.1e-78:389:97
 AJ007581

30

R-HEMBA1006724
 HS_2052_B1_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
 Plate=2052 Col=15 Row=F, genomic survey sequence.
 2.6e-46:309:88
 AQ305998

35

R-HEMBA1006749
 Homo sapiens mRNA for matrilin-4, partial.
 3.2e-88:472:94
 AJ007581

40

R-HEMBA1006770
 Homo sapiens CAGH4 mRNA, partial cds.
 6.5e-25:145:82
 U80746

45

R-HEMBA1006902
 Homo sapiens mRNA for matrilin-4, partial.
 9.3e-112:540:98
 AJ007581

50

R-HEMBA1006912
 ***ALU WARNING: Human Alu-Sc subfamily consensus sequence.
 6.6e-48:279:92
 U14571

55

R-HEMBA1006916
 Homo sapiens Grb14 mRNA, complete cds.

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- 1.8e-114:346:99
L76687
- 5 R-HEMBA1006960
Homo sapiens chromosome 19, cosmid F16403, complete sequence.
0.78:203:62
AC005777
- 10 R-HEMBA1007013
Human mRNA for DNA-binding protein TAXREB302, complete cds.
6.3e-31:163:100
D28468
- 15 R-HEMBA1007057
CIT-HSP-517F5.TP CIT-HSP Homo sapiens genomic clone 517F5, genomic survey sequence.
1.0:128:67
B49904
- 20 R-HEMBA1007063
Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein
S6 kinase, EST, GSS, STS. CpG island, complete sequence.
5.0e-43:300:88
AL022069
- 25 R-HEMBA1007241
HIV-1 RNA V3 region (patient Y, sample Y1, clone 05).
0.74:148:66
Z47529
- 30 R-HEMBA1007291
Homo sapiens chromosome 19, fosmid 37502, complete sequence.
3.6e-36:300:80
AC004755
- 35 R-HEMBA1007332
Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.
7.3e-15:148:80
U56430
- 40 R-HEMBB1000106
Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's.
8.0e-05:313:60
L40609
- 45 R-HEMBB1000276
HS_3048_A2_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
Plate=3048 Col=14 Row=E, genomic survey sequence.
0.91:234:58
AQ099411
- 50 R-HEMBB1000309
- R-HEMBB1000407
Mus musculus clone OST5976, genomic survey sequence.
- 55 6.4e-28:226:81
AF046768
- R-HEMBB1000447

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- Homo sapiens JWA protein mRNA, complete cds.
1.7e-107:533:97
AF070523
- 5 R-HEM BB1000542
Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.
4.4e-72:547:80
AF084259
- 10 R-HEM BB1000567
Human insulin-like growth factor (IGF-II) gene, exon 1 of 4.
4.3e-60:368:88
M13970
- 15 R-HEM BB1000642
Human DNA sequence from PAC 46H23, BRCA2 gene region chromosome 13q12-13 contains Klotho, ESTs.
2.9e-42:431:75
Z84483
- 20 R-HEM BB1000668
CITBI-E1-2508D15.TR CITBI-E1 Homo sapiens genomic clone 2508D15, genomic survey sequence.
2.5e-40:249:91
AQ261535
- 25 R-HEM BB1000679
HS_3061_A1_C03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061
Col=5 Row=E, genomic survey sequence.
1.8e-48:257:96
AQ127602
- 30 R-HEM BB1000881
CIT-HSP-2350020.TR CIT-HSP Homo sapiens genomic clone 2350020, genomic survey sequence.
0.0072:248:61
AQ062620
- 35 R-HEM BB1000905
Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.
2.5e-104:547:94
AC005089
- 40 R-HEM BB1001026

R-HEM BB1001048
- 45 R-HEM BB1001200
P.falciparum complete gene map of plastid-like DNA (IR-A).
1.5e-11:521:59
X95275
- 50 R-HEM BB1001407
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 2705, WORKING DRAFT SEQUENCE.
3.0e-29:308:77
AL033529
- 55 R-HEM BB1001530
Homo sapiens chromosome 19, cosmid R30538, complete sequence.
0.040:373:63
AC005943

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- 5 R-HEM BB1001547
Rickettsia prowazekii strain Madrid E, complete genome; segment 1/4.
0.027:291:62
AJ235270
- 10 R-HEM BB1001573
CIT-HSP-2307C1.TR CIT-HSP Homo sapiens genomic clone 2307C1, genomic survey sequence.
1.3e-13:90:98
AQ020395
- 15 R-HEM BB1001847
Homo sapiens chromosome 21q22.3 PAC 21L13, complete sequence.
3.4e-27:147:80
AF064864
- 20 R-HEM BB1001959
Homo sapiens clone 24781 mRNA sequence.
4.4e-103:504:97
AF070640
- 25 R-HEM BB1001978
CIT-HSP-2328G6.TF CIT-HSP Homo sapiens genomic clone 2328G6, genomic survey sequence.
7.9e-29:220:86
AQ040310
- 30 R-HEM BB1002039
Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.
2.7e-37:550:68
AC005014
- 35 R-HEM BB1002041
Sequence 1 from patent US 5633147.
2.7e-23:322:70
I43819
- 40 R-HEM BB1002051
Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.
9.2e-35:302:79
AC004825
- 45 R-HEM BB1002120
Homo sapiens Xp22 GS-524I1 (Genome Systems Human BAC library), complete sequence.
6.0e-05:479:59
AC003106
- 50 R-HEM BB1002162
Human DNA sequence from clone 739H11 on chromosome 1p33-34.2 Contains KIAA0237 gene, EST, STS, GSS,
complete sequence.
3.7e-30:238:84
AL031289
- 55 R-HEM BB1002228
Homo sapiens BAC clone NH0436H22 from 2, complete sequence.
6.6e-57:274:86
AC005234
- R-HEM BB1002245
Sequence 25 from patent US 5747660.

- 4.8e-30:361:73
AR005295
- 5 R-HEMBB1002302
Methanococcus jannaschii section 84 of 150 of the complete genome.
0.00019:362:59
U67542
- 10 R-HEMBB1002427
Genomic sequence from Human 9q34, complete sequence.
3.9e-105:533:96
AC001643
- 15 R-HEMBB1002465
Plasmodium falciparum chromosome 2, section 19 of 73 of the complete sequence.
2.9e-05:335:62
AE001382
- 20 R-HEMBB1002661
- R-HEMBB1002663
***ALU WARNING: Human Alu-Sq subfamily consensus sequence.
8.3e-43:268:89
U14573
- 25 R-HEMBB1002693
Human BAC clone RG126M09 from 7q21-q22, complete sequence.
2.4e-24:220:76
AC002067
- 30 R-MAMMA1000046
Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8
unordered pieces.
0.032:402:57
AC005505
- 35 R-MAMMA1000102
Human DNA sequence from cosmid B33F2 on chromosome 22 Contains ESTs.
2.0e-84:428:96
Z79996
- 40 R-MAMMA1000106
Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.
0.095:138:66
AP000031
- 45 R-MAMMA1000118
- R-MAMMA1000141
Homo sapiens 12q24.2 PAC RPC11-128M12 (Roswell Park Cancer Institute Human PAC library) complete se-
quence.
9.0e-91:480:95
AC004024
- 55 R-MAMMA1000204
Homo sapiens mRNA for LGMD2B protein.
1.5e-107:544:96
AJ007670

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- 5 R-MAMMA1000226
H.sapiens VASP gene, exons 4 to 13.
0.99:244:63
X98534
- 10 R-MAMMA1000403
CIT-HSP-2372A15.TF CIT-HSP Homo sapiens genomic clone 2372A15, genomic survey sequence.
8.0e-38:187:81
AQ112406
- 15 R-MAMMA1000449
Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.
1.2e-41:422:76
AC004491
- 20 R-MAMMA1000457
Homo sapiens clone 638 unknown mRNA, complete sequence.
7.4e-116:570:97
AF091084
- 25 R-MAMMA1000473
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.
9.6e-09:136:77
AC004131
- 30 R-MAMMA1000496
Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.
2.6e-48:272:93
AC004997
- 35 R-MAMMA1000528
Human BAC clone RG114A06 from 7q31, complete sequence.
1.8e-13:109:80
AC002542
- 40 R-MAMMA1000591
Human cosmid g1572c264, complete sequence.
1.6e-22:329:71
AC000359
- 45 R-MAMMA1000614
- 50 R-MAMMA1000652
H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA28A10.
0.81:158:65
Z84499
- 55 R-MAMMA1000681
Homo sapiens full length insert cDNA clone YY85D04.
1.0e-107:560:94
AF088014
- R-MAMMA1000706
Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.
1.1e-46:232:100
AF067223
- R-MAMMA1000788

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Bos taurus P14 (p14) mRNA, complete cds.
3.8e-72:493:84
AF037349

5 R-MAMMA1000810
Human DNA from overlapping chromosome 19-specific cosmids R29515 and R28253, genomic sequence, complete sequence.
5.0e-37:318:79
AC003002

10 R-MAMMA1000814
Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.
7.7e-15:140:85
AC003071

15 R-MAMMA1000881
Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.
8.8e-46:457:75
20 AL031311

R-MAMMA1000986
Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence.
7.7e-44:343:82
25 AF001550

R-MAMMA1000994
Homo sapiens mRNA for ISLR, complete cds.
3.6e-108:552:96
30 AB003184

R-MAMMA1001043

R-MAMMA1001066
35 Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.
1.3e-42:302:82
AC006120

R-MAMMA1001094
40 Homo sapiens clone 243 unknown mRNA, complete sequence.
5.4e-115:567:97
AF091094

R-MAMMA1001141
45 HS_3059_B1_H06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3059 Col=11 Row=P, genomic survey sequence.
1.3e-68:388:92
AQ214896

50 R-MAMMA1001150
H.sapiens mRNA for protein kinase C mu.
5.4e-20:340:66
X75756

55 R-MAMMA1001237
Mouse DNA fragment that hybridizes to HSV- 1 SmaI A fragment.
0.15:222:65
M11041

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- 5 R-MAMMA1001284
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SE-
QUENCE.
1.2e-33:344:76
AL034423
- 10 R-MAMMA1001310
Human Bruton agammaglobulinemia (BTK) gene, exons 10-12.
1.8e-39:332:80
L31565
- 15 R-MAMMA1001418
Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.
4.4e-42:411:76
U07563
- 20 R-MAMMA1001532
Homo sapiens PAC clone DJ0728D04, complete sequence.
2.3e-10:196:73
AC004865
- 25 R-MAMMA1001609
HS-1054-B2-H01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 776 Col=2
Row=P, genomic survey sequence.
1.6e-34:170:79
B42016
- 30 R-MAMMA1001615
- 35 R-MAMMA1001623
Homo sapiens 12q24.2 BAC RPC11-407A16 (Roswell Park Cancer Institute Human BAC Library) complete se-
quence.
8.8e-21:180:82
AC006065
- 40 R-MAMMA1001634
Homo sapiens chromosome 17, clone hRPK.85_B_7, complete sequence.
2.6e-40:283:86
AC005695
- 45 R-MAMMA1001893
Homo sapiens clone DJ0782K24, WORKING DRAFT SEQUENCE, 16 unordered pieces.
0.73:132:67
AC006003
- 50 R-MAMMA1001901
Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG
island.
4.0e-43:288:77
Z93023
- 55 R-MAMMA1001957
Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence.
1.2e-41:298:86
AC005212
- R-MAMMA1001978

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- R-MAMMA1002070
Homo sapiens clone DJ400N23, WORKING DRAFT SEQUENCE, 10 unordered pieces.
2.1e-104:530:97
AC005003
- 5 R-MAMMA1002080 rah=ras-related homolog [mice, HT4 neural cell line, mRNA, 993 nt].
5.9e-47:449:76
S72304
- 10 R-MAMMA1002087
Human Cosmid g1572c037 from 7q31.3, complete sequence.
1.7e-11:120:83
AC000125
- 15 R-MAMMA1002095
Rat alternatively spliced mRNA.
5.3e-30:289:74
M93018
- 20 R-MAMMA1002128

R-MAMMA1002142

R-MAMMA1002165
- 25 Homo sapiens chromosome 10 clone CIT987SK-1109P11, complete sequence.
1.1e-28:350:72
AC005871
- 30 R-MAMMA1002205
Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NUCLEIC ACID BINDING
PROTEIN (CNBP) like gene and STSs.
1.2e-42:282:75
Z83843
- 35 R-MAMMA1002224
Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSAII project).
0.99:210:60
AL022224
- 40 R-MAMMA1002234
Canine mRNA for 68kDA subunit of signal recognition particle (SRP68).
1.7e-61:310:81
X53744
- 45 R-MAMMA1002586
Streptomyces collinus coenzyme B12-dependent mutase (meaA) gene, complete cds.
0.99:348:60
AF008569
- 50 R-MAMMA1002633
Homo sapiens, clone hRPK. 1_A_1, complete sequence.
2.6e-13:381:64
AC006196
- 55 R-MAMMA1003126

R-NT2RM4000100
Plasmodium falciparum MAL3P2, complete sequence.

- 0.00047:296:61
AL034558
- 5 R-NT2RM4000115
Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P3, WORKING DRAFT SE-
QUENCE.
0.079:270:64
AL031746
- 10 R-NT2RM4000198
Homo sapiens chromosome 10 clone LA10NC01_15_E_11 map 10q26.3, WORKING DRAFT SEQUENCE, 3 un-
ordered pieces.
7.7e-24:244:78
AC006171
- 15 R-NT2RM4000284
Human IgG Fc receptor hFcRn mRNA, complete cds.
1.7e-93:440:100
U12255
- 20 R-NT2RM4000295
, complete sequence.
0.89:351:58
AC005663
- 25 R-NT2RM4000326
Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterra-
nean Fever gene disease.
2.3e-112:602:94
- 30 AJ003147
- R-NT2RM4000417
Human DNA sequence from PAC 326L13 containing brain-4 mRNA ESTs and polymorphic CA repeat.
0.78:229:62
- 35 Z82170
- R-NT2RM4000444
- R-NT2RM4000587
- 40 R-NT2RM4000593
- R-NT2RM4000648
0.010:260:61
- 45 AG005508
- R-NT2RM4000761
H.sapiens mitochondrial genome (consensus sequence).
3.2e-95:476:97
- 50 X62996
- R-NT2RM4000965
- R-NT2RM4000997
- 55 R-NT2RM4001321
Human DNA sequence from clone 1177E19 on chromosome 1p36.12-36.31. Contains the 3'part of the DNA-bind-
ing Zinc finger protein RIZ gene, ESTs, an STS, GSSs and a CpG island, complete sequence.

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6.0e-19:282:73
AL031277

R-NT2RM4001325

5

R-NT2RM4001377
Homo sapiens mRNA for KIAA0638 protein, partial cds.
2.9e-111:553:96
AB014538

10

R-NT2RM4001735
Homo sapiens clone 23904 mRNA sequence.
4.6e-106:553:94
AF052129

15

R-NT2RM4001768
Human HepG2 3'region Mbol cDNA, clone hmd3c03m3.
4.1e-29:187:91
D17194

20

R-NT2RM4001843
Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.
0.95:366:58
AC005828

25

R-NT2RM4002352
Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds.
5.5e-108:557:95
AB009462

30

R-NT2RP2000092
HS_3070_B1_B04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3070
Col=7 Row=D, genomic survey sequence.
1.1e-23:247:77
AQ120714

35

R-NT2RP2000178
E.amylovora lon gene.
1.1e-15:422:62
X77706

40

R-NT2RP2000240
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0539L10; HTGS phase 1,
WORKING DRAFT SEQUENCE, 15 unordered pieces.
0.00010:260:62
AC004480

45

R-NT2RP2000394
HS_3211_B2_G06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3211
Col=12 Row=N, genomic survey sequence.
1.1e-61:316:97
AQ174850

50

R-NT2RP2000447
Homo sapiens clone DJ1129D05, complete sequence.
8.7e-67:357:94
AC005630

55

- 5 R-NT2RP2000479
Homo sapiens chromosome 17, clone 193h18, complete sequence.
5.7e-51:551:73
AC002546
- 10 R-NT2RP2000514
P.falciparum parasite antigen reactive with the parasite inhibitory mouse monoclonal antibody (mMAb) 43E5, clone #366, partial cds.
2.1e-08:192:68
M21323
- 15 R-NT2RP2000533
Mus musculus cornichon mRNA, complete cds.
3.5e-59:243:82
AF022811
- 20 R-NT2RP2000616
Human DNA sequence from clone 694E4 on chromosome 22 Contains exon similar to phosphatidylserine decarboxylase, EST, GSS, complete sequence.
0.0064:105:67
AL031255
- 25 R-NT2RP2000649
Homo sapiens mRNA for Hs Ste24p, complete cds.
1.4e-65:326:98
AB016068
- 30 R-NT2RP2000663
Human DNA sequence from cosmid U61B11, between markers DXS366 and DXS87 on chromosome X contains ESTs.
7.9e-110:555:96
Z73913
- 35 R-NT2RP2000712
Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.
9.8e-32:308:78
AC006001
- 40 R-NT2RP2000739
Bos taurus TATA box binding protein (TBP) gene, partial cds.
0.19:128:68
L47974
- 45 R-NT2RP2000818
Caenorhabditis elegans cosmid C48D5, complete sequence.
0.010:429:58
Z36237
- 50 R-NT2RP2000903
H.sapiens 5T4 gene for 5T4 Oncofetal antigen.
4.0e-99:505:96
Z29083
- 55 R-NT2RP2001200
Homo sapiens mRNA for KIAA0676 protein, partial cds.
2.0e-57:306:95
AB014576

R-NT2RP2001223

R-NT2RP2001276
 Mouse regulatory protein (npdc-1) mRNA, complete cds.
 5.8e-14:353:65
 L03814

R-NT2RP2001388
 Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.
 1.7e-31:291:77
 AC004971

R-NT2RP2001469
 M.musculus tex292 mRNA (3'region).
 3.7e-26:188:89
 X80433

R-NT2RP2001480
 Homo sapiens thrombospondin 3 (THBS3) gene, complete cds.
 6.6e-83:426:95
 L38969

R-NT2RP2001495
 transcript ch123.Rev [human, RF1,RF48 stomach cancer cell lines, mRNA, 252 nt].
 6.3e-43:238:96
 S77359

R-NT2RP2001514
 Homo sapiens cyclin K (CPR4) mRNA, complete cds.
 6.6e-06:57:100
 AF060515

R-NT2RP2001538
 Mus musculus transcriptional regulatory protein (mSin3) gene, complete cds.
 6.9e-12:179:75
 L36831

R-NT2RP2001562
 Human PAC clone DJ0800B09 from 7q11.23-q21, complete sequence.
 0.074:257:61
 AC004028

R-NT2RP2001662
 Homo sapiens clone 24615 mRNA sequence.
 3.2e-94:485:95
 AF055012

R-NT2RP2001755
 Homo sapiens mRNA for KIAA0762 protein, partial cds.
 1.3e-103:576:92
 AB018305

R-NT2RP2001769
 CIT-HSP-2376O23.TF CIT-HSP Homo sapiens genomic clone 2376023, genomic survey sequence.
 1.5e-74:381:96
 AQ111163

R-NT2RP2001817

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100

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Z98597

R-NT2RP2002510

Homo sapiens chromosome 19, cosmid F19847, complete sequence.

1.6e-38:307:81

AC005952

R-NT2RP2002527

Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene, complete sequence.

1.5e-18:165:83

AC004770

R-NT2RP2002533

Homo sapiens alpha 2 delta calcium channel subunit isoform II mRNA, complete cds.

9.7e-116:580:96

AF042793

R-NT2RP2002564

Homo sapiens clone DJ0800G07, complete sequence.

3.8e-110:580:94

AC004890

R-NT2RP2002674

Plasmodium falciparum chromosome 2, section 11 of 73 of the complete sequence.

1.0:244:60

AE001374

R-NT2RP2002721

Homo sapiens chromosome 17, clone HCIT217L10, complete sequence.

1.2e-10:221:73

AC003962

R-NT2RP2002824

Human HepG2 3' region Mbol cDNA, clone hmd4f06m3.

3.0e-07:108:77

D17237

R-NT2RP2002942

Human DNA sequence from clone 88D7 on chromosome Xq25-26.3 Contains F9 (coagulation factor IX (plasma thromboplastic component, Christmas disease, haemophilia B)), dbl oncogene. EST, STS, GSS, complete sequence.

2.0e-37:491:71

AL033403

R-NT2RP2002974

H.sapiens DMAHP gene.

4.0e-118:585:97

X84813

R-NT2RP2002976

CIT-HSP-2348J20.TF CIT-HSP Homo sapiens genomic clone 2348J20, genomic survey sequence.

8.4e-45:233:98

AQ059444

R-NT2RP2003042

R-NT2RP2003179

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R-NT2RP2003210

R-NT2RP2003302

Human DNA sequence from 4PTL, Huntington's Disease Region, chromosome 4p16.3.

1.5e-24:255:78

Z95704

R-NT2RP2003369

Homo sapiens chromosome 7q22 sequence, complete sequence.

3.1e-95:514:92

AF053356

R-NT2RP2003383

Homo sapiens mRNA for KIAA0458 protein, complete cds.

3.9e-111:549:97

AB007927

R-NT2RP2003390

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191J18, WORKING DRAFT SEQUENCE.

4.9e-102:413:99

AL024507

R-NT2RP2003469

Genomic sequence from Human 9q34, complete sequence.

1.4e-35:376:74

AC001644

R-NT2RP2003545

Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.

1.5e-09:503:61

AL034557

R-NT2RP2003593

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 971N18, WORKING DRAFT SEQUENCE.

7.8e-81:433:93

AL021396

R-NT2RP2003599

HS_3240_A1_C04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3240 Col=7 Row=E, genomic survey sequence.

0.091:341:58

AQ206348

R-NT2RP2003655

Homo sapiens PAC clone DJ0015123 from 22, complete sequence.

2.0e-08:249:69

AC004819

R-NT2RP2003664

Homo sapiens mRNA for leptin receptor gene-related protein.

1.7e-110:549:96

Y12670

R-NT2RP2003931

Human mRNA for KIAA0365 gene, partial cds.

5.4e-112:571:96

AB002363

R-NT2RP2003940

Human Chromosome 11 pac pDJ1173a5, complete sequence.

2.4e-20:353:70

AC000378

R-NT2RP2003950

Homo sapiens clone 24778 unknown mRNA.

1.5e-96:494:95

AF070572

R-NT2RP2004069

Human DNA sequence from clone 618F1 on chromosome Xq25 Contains part of gene similar to DOC4, CA repeat, GSS, complete sequence.

2.6e-50:539:75

AL023878

R-NT2RP2004108

RPCII1-91F9.TV RPCI11 Homo sapiens genomic clone R-91F9, genomic survey sequence. 0.00013:281:63

AQ283338

R-NT2RP2004141

cSRL-115f11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-115f11, genomic survey sequence.

2.3e-05:239:64

B00539

R-NT2RP2004179

Genomic sequence from Human 9q34, complete sequence.

0.43:130:68

AC002322

R-NT2RP2004205

Homo sapiens chromosome 7q22 sequence, complete sequence.

1.4e-42:324:83

AF053356

R-NT2RP2004447

Homo sapiens Chromosome 11q13 BAC Clone 18h3, WORKING DRAFT SEQUENCE, 7 ordered pieces.

5.5e-35:285:84

AC000353

R-NT2RP2004495

transcript ch123.Rev [human, RF1, RF48 stomach cancer cell lines, mRNA, 252 nt].

3.4e-44:238:97

S77359

R-NT2RP2004524

Genomic sequence from Human 9q34, complete sequence.

7.4e-113:572:96

AC001644

R-NT2RP2004556

CIT-HSP-2306F6.TF CIT-HSP Homo sapiens genomic clone 2306F6, genomic survey sequence.

8.1e-99:514:95

AQ019229

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- R-NT2RP2004606 cDNA encoding NIC(Natural Inhibitor of Collagenase).
8.2e-116:576:96
E00985
- 5 R-NT2RP2004648
Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.
0.98:369:57
AC005828
- 10 R-NT2RP2004670
Rattus norvegicus vesicla-associate calmodulin-binding protein mRNA, complete cds.
4.5e-43:592:69
L22557
- 15 R-NT2RP2004794
R-NT2RP2004837
Human Chromosome 11 pac pDJ148f1, WORKING DRAFT SEQUENCE, 27 unordered pieces.
1.2e-60:366:90
20 AC001232
- R-NT2RP2004847
Homo sapiens full length insert cDNA clone YY87C09.
1.0e-68:333:100
25 AF086055
- R-NT2RP2005027
Human glucose transporter-like protein-III (GLUT3), complete cds.
7.8e-103:508:97
30 M20681
- R-NT2RP2005069
Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.
3.8e-42:463:73
35 U35245
- R-NT2RP2005163
CIT-HSP-2348J20.TF CIT-HSP Homo sapiens genomic clone 2348J20, genomic survey sequence.
7.4e-44:233:96
40 AQ059444
- R-NT2RP2005181
Rattus norvegicus mRNA for cationic amino acid transporter 3, complete cds.
7.6e-53:567:73
45 AB000113
- R-NT2RP2005247
Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC RPCI1-93D11 (from Roswell
Park Cancer Center) complete sequence.
50 5.8e-38:341:76
AC002357
- R-NT2RP2005378
Homo sapiens full length insert cDNA clone YW25A12.
55 0.13:152:66
AF086029
- R-NT2RP2005391

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HS_3056_A1_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
Plate=3056 Col=5 Row=E, genomic survey sequence.

1.1e-14:140:84

AQ134064

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R-NT2RP2005425

Homo sapiens mRNA for KIAA0803 protein, partial cds.

8.2e-100:526:94

AB018346

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R-NT2RP2005463

R-NT2RP2005514

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R-NT2RP2005535

Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.

1.9e-11:488:62

AC003973

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R-NT2RP2005541

CIT-HSP-2034G23.TF CIT-HSP Homo sapiens genomic clone 2034G23, genomic survey sequence.

2.7e-61:311:98

B74709

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R-NT2RP2005597

R-nnnnnnnnnnnnn

{FRA16A, folate-sensitive fragile site} [human, Genomic, 160 nt].

0.92:104:65

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S70397

R-NT2RP2005666

R-NT2RP2005774

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Homo sapiens apoptosis-related mRNA, 3'UTR, partial sequence.

2.2e-94:440:96

AF035364

R-NT2RP2005878

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Homo sapiens chromosome 19, cosmid F17987, complete sequence.

1.3e-32:340:76

AC004790

R-NT2RP2005883

45

Human DNA sequence from clone 248E1 on chromosome 6q23.1-23.3 Contains DOPAMINE-BETA-MONOOXY-
GENASE PRECURSOR, EF-1-ALPHA-2 pseudogene EST GSS and CA repeat, complete sequence.

1.3e-117:581:97

AL023578

50

R-NT2RP2005887

Human Chromosome 11 pac pDJ148f1, WORKING DRAFT SEQUENCE, 27 unordered pieces

2.5e-61:367:90

AC001232

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R-nnnnnnnnnnnnn

Human paired box gene (PAX6) homologue, complete cds.

5.0e-115:578:96

M93650

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- 5 R-NT2RP2005994
Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.
2.4e-116:594:96
AC004050
- 10 R-NT2RP2006004
Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.
1.8e-45:264:93
U42975
- 15 R-NT2RP2006042
T31H24TF TAMU Arabidopsis thaliana genomic clone T31H24, genomic survey sequence.
0.42:111:70
B78148
- 20 R-NT2RP2006092
Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.
1.7e-73:385:95
AC005214
- 25 R-NT2RP2006099
Homo sapiens PAC clone DJ0903G02, complete sequence.
1.3e-27:335:74
AC004924
- 30 R-NT2RP2006134
Homo sapiens chromosome 4 clone B139M23 map 4q25, complete sequence.
1.0:143:63
AC004045
- 35 R-NT2RP2006269
Phreatamoeba balamuthi UBI3 sequence, putative polyubiquitin gene.
0.82:153:63
AJ000657
- 40 R-NT2RP2006512
Homo sapiens clone 23904 mRNA sequence.
4.6e-106:531:96
AF052129
- 45 R-NT2RP3000011
HS_2196_A2_E08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196
Col=16 Row=I, genomic survey sequence.
1.3e-36:292:83
AQ210450
- 50 R-NT2RP3000022
Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-15, complete sequence.
0.28:248:60
Z98550
- 55 R-NT2RP3000059
Homo sapiens chick ovalbumin upstream promoter transcription factor II (COUP-TFII) mRNA, partial cds.
0.047:393:61
M62760
- R-NT2RP3000063
HS_3190_B2_D10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone

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Plate=3190 Col=20 Row=H, genomic survey sequence.
0.88:232:63
AQ172428

- 5 R-nnnnnnnnnnnnn
RPC111-35A1.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-35A1, genomic survey sequence.
3.8e-29:159:99
AQ045699
- 10 R-NT2RP3000148
Homo sapiens full length insert cDNA clone ZE03A07.
2.8e-112:574:95
AF086510
- 15 R-NT2RP3000169
Homo sapiens MRS1 mRNA, complete cds.
4.4e-110:551:96
AF093239
- 20 R-NT2RP3000171

R-NT2RP3000172
Rattus norvegicus vesicla-associate calmodulin-binding protein mRNA, complete cds.
1.3e-40:554:70
L22557
- 25

R-NT2RP3000201
Homo sapiens BAC clone NH0353P23 from 2, complete sequence.
6.4e-96:478:97
AC005035
- 30

R-NT2RP3000232
Plasmodium falciparum MAL3P2, complete sequence.
0.93:262:61
AL034558
- 35

R-NT2RP3000304
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.
2.4e-109:546:97
AF074264
- 40

R-NT2RP3000378
Mus musculus mSin3A (sin3A) mRNA, complete cds.
3.0e-27:411:72
U22394
- 45

R-NT2RP3000436
Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.
1.1e-06:440:57
AE001398
- 50

R-NT2RP3000444
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 889J22, WORKING DRAFT SEQUENCE.
5.9e-105:543:95
AL031406
- 55

R-NT2RP3000460
Canis familiaris sec61 homologue mRNA, complete cds.

- 2.8e-12:292:68
M96629
- 5 R-NT2RP3000481
WORKING DRAFT SEQUENCE, 8 unordered pieces.
0.99:160:65
AC005992
- 10 R-NT2RP3000616
Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5
unordered pieces.
0.00087:412:57
AC005308
- 15 R-NT2RP3000645
- R-NT2RP3000652
Homo sapiens DNA from chromosome 19, cosmid R32532, complete sequence.
1.9e-44:539:74
20 AC004004
- R-NT2RP3000676
Homo sapiens mRNA for KIAA0446 protein, complete cds.
3.1e-103:542:94
25 AB007915
- R-NT2RP3000677
Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 4/10.
0.067:235:61
30 AB020872
- R-NT2RP3000721
CIT-HSP-2348J20.TF CIT-HSP Homo sapiens genomic clone 2348J20, genomic survey sequence.
4.0e-45:233:98
35 AQ059444
- R-NT2RP3000789
- R-NT2RP3000818
40 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 94M16, WORKING DRAFT SEQUENCE.
5.7e-95:510:93
Z97201
- R-NT2RP3000820
45 RPCI11-77B13.TJ RPCI11 Homo sapiens genomic clone R-77B13, genomic survey sequence.
2.1e-50:266:96
AQ283547
- R-NT2RP3000838
50 Homo sapiens mRNA for KIAA0638 protein, partial cds.
4.6e-99:522:94
AB014538
- R-NT2RP3000871
55 Homo sapiens clone DJ0703P08, WORKING DRAFT SEQUENCE, 23 unordered pieces.
0.68:249:61
AC005481

- 5 R-NT2RP3000907
X.laevis oocyte repetitive sequence (XLOREP) mRNA.
2.9e-30:386:69
X65290
- 10 R-NT2RP3000921
HS_2026_A1_B06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026
Col=11 Row=C, genomic survey sequence.
2.2e-54:311:92
AQ232644
- 15 R-NT2RP3001012
Rattus norvegicus mRNA for TIP120, complete cds.
9.2e-63:456:83
D87671
- 20 R-NT2RP3001044
Human Chromosome 11 pac pDJ148f1, WORKING DRAFT SEQUENCE, 27 unordered pieces.
1.2e-60:366:90
AC001232
- 25 R-NT2RP3001061
Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7
unordered pieces.
0.17:357:61
AC005506
- 30 R-NT2RP3001159
Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH),
complete sequence.
8.8e-111:561:96
AC004228
- 35 R-NT2RP3001170
Homo sapiens mRNA for KIAA0784 protein, partial cds.
8.8e-117:561:98
AB018327
- 40 R-NT2RP3001195
Genomic sequence from Human 9q34, complete sequence.
1.4e-35:376:74
AC001644
- 45 R-NT2RP3001240
Canis familiaris sec61 homologue mRNA, complete cds.
2.8e-12:292:68
M96629
- 50 R-NT2RP3001271
Homo sapiens chromosome 19, BAC CIT-B-470f8 (BC330812), complete sequence.
7.9e-17:260:71
AC006115
- 55 R-NT2RP3001322
Human DNA sequence from PAC 128N22 on chromosome Xq25-Xq26.3. contains STS.
0.035:451:60
Z97629

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- 5 R-NT2RP3001542
Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.
4.1e-08:500:61
AC004153
- 10 R-NT2RP3001560
Mouse mRNA for thymic epithelial cell surface antigen, complete cds.
1.0e-30:523:65
D67067
- R-NT2RP3001592
- 15 R-NT2RP3001685
Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.
2.4e-30:147:85
AL024474
- 20 R-NT2RP3001738
Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.
9.2e-107:553:95
AC004228
- 25 R-NT2RP3001754
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.
2.0e-67:345:97
AL034380
- 30 R-NT2RP3001858
- R-NT2RP3001976
Homo sapiens chromosome 9, clone hRPK.467_F_21, complete sequence.
35 4.4e-14:302:62
AC006239
- R-NT2RP3002015
Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.
40 6.2e-65:492:82
AC004832
- R-NT2RP3002160
Genomic sequence from Human 9q34, complete sequence.
45 2.1e-82:431:95
AC001643
- R-NT2RP3002281
Homo sapiens mRNA for KIAA0765 protein, partial cds.
50 1.1e-81:446:93
AB018308
- R-NT2RP3002286
Mus musculus EGF repeat transmembrane protein mRNA, complete cds.
55 1.0e-80:378:90
U57368
- R-NT2RP3002311

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- Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.
0.57:366:58
AC005828
- 5 R-NT2RP3002324
H.sapiens gene for nitric oxide synthase (promoter region).
1.6e-30:337:72
Z49251
- 10 R-NT2RP3002342
transcript ch123.Rev [human, RF1,RF48 stomach cancer cell lines, mRNA, 252 nt].
6.5e-45:238:98
S77359
- 15 R-NT2RP3002353
Human Chromosome 16 BAC clone CIT987SK-A-418G10, complete sequence. 0.00015:164:70
AC002044
- 20 NNNNNNNNNNNNNNN
Homo sapiens mRNA for KIAA0788 protein, partial cds.
4.5e-98:493:96
AB018331
- 25 NNNNNNNNNNNNNNN
R-NT2RP3002448
S.cerevisiae DNA for ori 2.
0.52:91:71
X59535
- 30 R-NT2RP3002571
- 35 R-NT2RP3002664
Homo sapiens full length insert cDNA clone ZC48G09.
9.9e-103:522:96
AF086209
- R-NT2RP3002721
- 40 R-NT2RP3002737
- R-NT2RP3002738
Sequence 4 from patent US 5541109.
2.9e-22:171:74
- 45 I24014
- R-NT2RP3002790
- 50 R-NT2RP3002836
Bos taurus retina specific RGS protein (RET-RGS1) mRNA, complete cds.
2.3e-34:384:75
U89254
- 55 R-NT2RP3002887
Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.
1.6e-05:435:62
AF051726

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R-NT2RP3003559
 CIT-HSP-2307F17.TR CIT-HSP Homo sapiens genomic clone 2307F17, genomic survey sequence.
 1.4e-15:342:68
 AQ016972

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R-NT2RP3003614
 Homo sapiens chromosome 19, cosmid F21967, complete sequence.
 0.013:174:64
 AC005256

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R-NT2RP3003729

 R-NT2RP3003849
 Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE, 6 unordered pieces.
 8.9e-106:557:94
 AC002320

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R-NT2RP3003874
 Homo sapiens incomplete cDNA for a mutated allele of a myosin class I, myh-1c.
 1.6e-55:302:94
 AJ001381

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R-NT2RP3003963
 cSRL-66f9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-66f9, genomic survey sequence.
 0.028:78:76
 B05608

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R-NT2RP3004000
 Tapa-1=integral membrane protein TAPA-1 [mice, B cell lymphoma line 38C13, Genomic, 861 nt, segment 7 of 7].
 0.87:212:62
 S45012

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R-NT2RP3004025
 Homo sapiens chromosome 19, cosmid F17987, complete sequence.
 0.71:197:62
 AC004790

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R-NT2RP3004075

 R-NT2RP3004083
 Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 5.
 0.27:375:59
 Z97340

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R-NT2RP3004090
 CIT-HSP-2172H20.TR CIT-HSP Homo sapiens genomic clone 2172H20, genomic survey sequence.
 2.2e-40:243:91
 B99962

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R-NT2RP3004119
 Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.
 8.3e-42:475:73
 AC004953

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R-NT2RP3004130

 R-NT2RP3004133

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CIT-HSP-2306G15.TR CIT-HSP Homo sapiens genomic clone 2306G15, genomic survey sequence.

0.00037:194:64

AQ022229

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R-NT2RP3004202

Homo sapiens BAC clone GS285F21 from 7q21-q22, complete sequence.

0.65:209:62

AC004012

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R-NT2RP3004294

R-NT2RP3004309

Homo sapiens Chromosome 11q12.2 PAC clone pDJ519o13 containing human gene for ferritin heavy chain (FTH), complete sequence.

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7.4e-99:500:96

AC004228

R-NT2RP3004321

Human chromosome 11 168h3 cosmid, complete sequence.

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1.7e-105:540:96

U73637

R-NT2RP3004345

Human BAC clone RG016J04 from 7q21, complete sequence.

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0.00033:348:61

AC002064

R-NT2RP3004355

Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.

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0.0029:180:66

AC004709

R-NT2RP3004374

Human DNA sequence from clone 1177E19 on chromosome 1p36.12-36.31. Contains the 3' part of the DNA-binding Zinc finger protein RIZ gene, ESTs, an STS, GSSs and a CpG island, complete sequence.

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4.3e-18:223:77

AL031277

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R-NT2RP3004406

Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-70, complete sequence.

1.0:201:62

AL010239

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R-NT2RP3004481

R-NT2RP3004552

Human germline immunoglobulin lambda light chain pseudogene (VII.1).

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1.0:165:63

X57825

R-NT2RP3004625

Homo sapiens I-1 receptor candidate protein mRNA, complete cds.

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8.2e-49:352:84

AF082516

R-NT2RP3004640

Homo sapiens full length insert cDNA clone ZC45E05.

- 1.2e-96:471:98
AF086205
- 5 R-NT2RP3004647
Homo sapiens mRNA for KIAA0446 protein, complete cds.
1.5e-109:555:96
AB007915
- 10 R-NT2RP4000108
Mouse neurofilament protein (NF-L) gene, 3' flank.
1.0e-09:344:63
M55424
- 15 R-NT2RP4000634
Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.
1.6e-16:267:71
AC003037
- 20 R-NT2RP4000962
Human DNA sequence from PAC 970D1 on chromosome 1q24. Contains ESTs, STSs and a BAC end-sequence (GSS).
0.026:176:67
AL021069
- 25 R-NT2RP4001001
Drosophila melanogaster Oregon-R mitochondrial A+T region.
0.00026:354:61
U11584
- 30 R-NT2RP4001009
Homo sapiens mRNA for Hs Ste24p, complete cds.
1.6e-82:408:98
AB016068
- 35 R-NT2RP4001467
Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).
1.8e-111:545:97
X55740
- 40 R-NT2RP4001877
Yeast (S.cerevisiae) mitochondrial cob gene, intron 4.
0.19:384:59
J01469
- 45 R-NT2RP4001879
Homo sapiens full length insert cDNA clone ZD76G10.
4.4e-107:548:94
AF086408
- 50 R-NT2RP4002187
RPC111-69F22.TK RPC111 Homo sapiens genomic clone R-69F22, genomic survey sequence.
7.1e-37:240:89
AQ238297
- 55 R-NT2RP4002451
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111B22, WORKING DRAFT SEQUENCE.
5.8e-111:575:96
Z98200

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- 5 R-NT2RP4002715
Human Chromosome 11 pac pDJ148f1, WORKING DRAFT SEQUENCE, 27 unordered pieces.
2.5e-61:367:90
AC001232
- 10 R-NT2RP4002750
Rattus norvegicus mRNA for cationic amino acid transporter 3, complete cds.
1.2e-52:527:74
AB000113
- 15 R-OVARC1000003
Homo sapiens clone DJ0856O24, WORKING DRAFT SEQUENCE, 4 unordered pieces.
2.3e-10:140:77
AC004909
- 20 R-OVARC1000090
Homo sapiens genomic DNA, 237 kb segment from 6p21.3 region including HLA genes, WORKING DRAFT SE-
QUENCE.
2.8e-59:323:78
D84394
- 25 R-OVARC1000105
H.sapiens gene for ribosomal protein L38.
2.7e-12:83:100
Z26876
- R-OVARC1000137
- 30 R-OVARC1000208
Homo sapiens PAC clone DJ0817I18 from 7p11.2p13, complete sequence.
2.7e-52:464:79
AC004901
- 35 R-OVARC1000255
H.sapiens syk mRNA for protein-tyrosine kinase.
1.9e-105:511:98
Z29630
- 40 R-OVARC1000275
- R-OVARC1000298
Plasmodium falciparum carbamoyl phosphate synthetase II gene, complete cds.
0.66:364:59
L32150
- 45 R-OVARC1000307
- R-OVARC1000313
Homo sapiens mRNA for KIAA0573 protein, partial cds.
1.6e-96:534:93
AB011145
- 50 R-OVARC1000331
Sequence 2 from patent US 5763589.
8.1e-66:335:97
AR012692
- 55 R-OVARC1000410

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Homo sapiens clone 23767 and 23782 mRNA sequences.

1.0e-88:462:94

AF007150

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R-OVARC1000439

E.coli fanG and fanH genes.

0.99:424:58

Y00531

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R-OVARC1000467

HS_3235_A2_A12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235

Col=24 Row=A, genomic survey sequence.

9.2e-09:125:76

AQ206826

15

R-OVARC1000529

R-OVARC1000553

Homo sapiens chromosome 19, cosmid R26894, complete sequence.

20

2.0e-84:437:96

AC005594

R-OVARC1000775

CIT-HSP-2060P5.TF CIT-HSP Homo sapiens genomic clone 2060P5, genomic survey sequence. 0.29:223:63

25

B70025

R-OVARC1000811

Homo sapiens chromosome 16, cosmid clone 432A1 (LANL), complete sequence.

2.8e-89:438:98

30

AC004235

R-OVARC1000853

RPCI11-16C11.TV RPCI-11 Homo sapiens genomic clone RPCI-11-16C11, genomic survey sequence.

5.3e-53:317:92

35

B76661

R-OVARC1000873

Human DNA sequence from clone 1049G16 on chromosome 20q12-13.2 Contains gene similar to GLU-COSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence.

40

1.2e-102:511:97

AL034418

R-OVARC1000916

H.sapiens PISSLRE mRNA.

45

5.8e-111:588:94

X78342

R-OVARC1000956

Human DNA sequence from cosmid L241B9, Huntington's Disease Region, chromosome 4p16.3 contains polymorphic VNTR pYNZ32.

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2.7e-89:478:94

Z69708

R-OVARC1000995

Human DNA sequence from clone 885E17 on chromosome 1p33-34.1. Contains STSs and GSSs and genomic marker D1S1302, complete sequence.

55

9.5e-46:325:84

AL031294

EP 1 130 094 A2

- 5 R-OVARC1001030
Homo sapiens neuroendocrine-specific protein C (NSP) mRNA, complete cds.
1.2e-05:197:63
L10335
- R-OVARC1001049
- 10 R-OVARC1001086
Homo sapiens cyclin T2a mRNA, complete cds.
4.3e-105:569:94
AF048731
- 15 R-OVARC1001132
Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.
2.2e- 111:569:96
AP000038
- 20 R-OVARC1001163
Sus scrofa MHC SLA class III steroid 21-hydroxylase (CYP21) gene, complete cds, ORF human-like gene, last 5 exons.
0.010:349:60
M83939
- 25 R-OVARC1001222
Spiroplasma citri orfa and orff genes, partial cds, orfb, orfc, and orfe genes and Spiroplasma virus SpV1-derived ORF1 and ORF3 genes, complete cds, and SpV1-derived ORF14 gene, partial cds.
0.58:184:60
U28972
- 30 R-OVARC1001260
Homo sapiens clone DJ0856O24, WORKING DRAFT SEQUENCE, 4 unordered pieces.
1.1e-10:140:78
AC004909
- 35 R-OVARC1001336
Homo sapiens clone DJ0856O24, WORKING DRAFT SEQUENCE, 4 unordered pieces.
2.3e-10:140:77
AC004909
- 40 R-OVARC1001338
- R-OVARC1001569
- 45 R-OVARC1001570
- R-OVARC1001596
Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.
5.9e-47:361:83
AC005951
- 50 R-OVARC1001607
Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.
3.3e-112:559:96
U15128
- 55 R-OVARC1001725
Homo sapiens patched related protein TRC8 (TRC8) gene, exon 1 and partial cds.
3.9e-56:318:95

- AF064800
- R-OVARC1001727
Human DNA sequence from clone 48A11 on chromosome 20p12 Contains EST, STS, GSS, complete sequence.
5 6.1e-101:533:94
AL031132
- R-OVARC1001807
Human TR3 orphan receptor mRNA, complete cds.
10 2.8e-87:426:97
L13740
- R-OVARC1001833
Mouse fork head related protein (HNF-3beta) mRNA, complete cds.
15 1.1e-21:263:76
L10409
- R-OVARC1001991
H.sapiens chromosome 22 CpG island DNA genomic Mse1 fragment, clone 301e3, reverse read 301e3.r.
20 0.90:151:59
Z79826
- R-OVARC1002058
Homo sapiens full length insert cDNA clone ZD58C02.
25 1.9e-105:547:95
AF088043
- R-OVARC1002178
Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and
30 a pseudogene, ESTs, STSs and GSSs, complete sequence.
0.26:429:58
AL031053
- R-PLACE1000033
35 Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4
unordered pieces.
0.098:467:59
AC004688
- R-PLACE1000231
40 Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.
0.91:141:64
AC003083
- R-PLACE1000258
45 Human DNA sequence from clone 710L4 on chromosome Xq11.2-12 Contains part of a gene similar to myotubu-
larin-related protein, EST, STS and GSS, complete sequence.
3.8e-53:524:75
AL034408
- R-PLACE1000442
50 Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K22F20, complete sequence.
3.0e-07:413:62
AB016873
- R-PLACE1000560
55 Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.
6.3e-59:323:94

- AC005368
- R-PLACE1000740
H.sapiens PEX gene.
5 0.0065:202:63
Y10196
- R-PLACE1000912
- 10 R-PLACE1000914
Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.
3.4e-68:452:86
AC002093
- 15 R-PLACE1000927
Cowpox virus strain GRI-90 DNA (49 kb fragment).
1.8e-46:432:76
Y15035
- 20 R-PLACE1000986
HS_2037_A2_B06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037
Col=12 Row=C, genomic survey sequence.
0.087:48:89
AQ232754
- 25 R-PLACE1001016
M.fascicularis gene for apolipoprotein A-IV.
0.016:226:61
X68361
- 30 R-PLACE1001100
Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear in-
hibitor of protein phosphatase-1, ESTs, and a CA repeat.
3.4e-37:320:80
- 35 AL020997
- R-PLACE1001114
RPC111-5C23.TV RPCI-11 Homo sapiens genomic clone RPCI-11-5C23, genomic survey sequence.
9.2e-44:173:85
- 40 B49180
- R-PLACE1001123
- R-PLACE1001183
45 Plasmodium falciparum MAL3P8, complete sequence.
0.47:217:63
AL034560
- R-PLACE1001229
50 Mitochondrion Culex torrentium A+T rich mitochondrial control region.
3.3e-09:356:63
U69573
- R-PLACE1001231
55 Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete cds.
1.2e-09:186:72
AF026554

5 R-PLACE1001340
Homo sapiens mRNA for KIAA0719 protein, complete cds.
2.0e-51:265:98
AB018262

10 R-PLACE1001401
Bactrocera dorsalis strain Tahiti mitochondrial D-loop region, complete sequence.
0.0073:203:60
AF033929

15 R-PLACE1001407
Human DNA sequence from clone 496H19 on chromosome 6q24 Contains ESTs, complete sequence.
5.8e-70:360:96
AL023582

20 R-PLACE1001464
Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).
3.1e-90:457:96
X55740

25 R-PLACE1001500
Homo sapiens clone DJ0917G04, WORKING DRAFT SEQUENCE, 35 unordered pieces.
1.0:232:62
AC004929

30 R-PLACE1001516
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-575C2, complete sequence.
1.9e-26:168:88
AC002425

35 R-PLACE1001536
Human Chromosome X clone bWXD187, complete sequence.
6.5e-61:310:98
AC004383

40 R-PLACE1001564
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 287G14, WORKING DRAFT SE-
QUENCE.
2.9e-100:504:97
AL033377

45 R-PLACE1001655
Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA, complete cds.
3.8e-1 17:578:97
AF043472

50 R-PLACE1001788
Sequence 9 from Patent WO9722695.
1.9e-05:91:82
A63556

55 R-PLACE1001795

R-PLACE1001836
, complete sequence.
4.1e-14:269:69
AC005406

EP 1 130 094 A2

- R-PLACE1001918
Human HepG2 3' region Mbol cDNA, clone hmd4f06m3.
7.3e-25:151:95
D17237
- 5 R-PLACE1001949
Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RS1 gene for retinoschisis (X-linked, juvenile) 1 (XLRS1). Contains ESTs, an STS and GSSs, complete sequence.
10 0.54:165:63
Z94056
- R-PLACE1002080
Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.
15 3.7e-60:289:95
AC004150
- R-PLACE1002095
Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-52, complete sequence.
20 0.00052:422:59
AL008982
- R-PLACE1002153
Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.
25 4.6e-100:514:95
AF095791
- R-PLACE1002329
Homo sapiens chromosome 19, cosmid R31855, complete sequence.
30 1.3e-46:257:95
AC005782
- R-PLACE1002355
HS_2057_B1_D01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2057
35 Col=1 Row=H, genomic survey sequence.
0.089:132:65
AQ245227
- R-PLACE1002374
Human mRNA for pro-cathepsin L (major excreted protein MEP).
40 2.6e-101:501:97
X12451
- R-PLACE1002518
HS_2176_A2_D04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone
45 Plate=2176 Col=8 Row=G, genomic survey sequence.
1.7e-43:221:100
AQ014851
- R-PLACE1002547
Homo sapiens mRNA for KIAA0719 protein, complete cds.
50 2.0e-53:276:97
AB018262
- R-PLACE1002726
Human DNA-binding protein ABP/ZF mRNA, complete cds.
55 1.1e-37:212:94
U82613

- R-PLACE1002905
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 215D11, WORKING DRAFT SE-
QUENCE.
1.2e-42:302:86
5 AL034417
- R-PLACE1002911
- R-PLACE1002967
10 Homo sapiens chromosome 16, BAC clone 461A8, complete sequence.
2.3e-39:310:82
AC006111
- R-PLACE1003135
15 Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SE-
QUENCE.
2.2e-07:418:60
AL034557
- R-PLACE1003163
20 Homo sapiens DBI-related protein mRNA, complete cds.
4.7e-110:547:96
AF069301
- R-PLACE1003407
25 Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds.
1.7e-47:287:91
AF068227
- R-PLACE1003428
30 Human DNA sequence from clone 55C23 on chromosome 6q22.3-23.3 contains vanin-like genes VNN1 and VNN2,
ESTs, GSSs., complete sequence.
1.1e-75:268:98
AL032821
- R-PLACE1003438
35
- R-PLACE1003460
40 HS_3026_B1_A08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026
Col=15 Row=B, genomic survey sequence.
0.30:100:69
AQ093523
- R-nnnnnnnnnnnnn
45 Homo sapiens clone DJ0981007, complete sequence.
3.3e-46:135:98
AC006017
- R-PLACE1003573
50 HS_3079_B2_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079
Col=4 Row=B, genomic survey sequence.
1.1e-49:261:96
AQ121751
- R-PLACE1003598
55
- R-PLACE1003644
Caenorhabditis elegans cosmid F52H3, complete sequence.

- 0.38:345:62
Z66512
- 5 R-PLACE1003737
Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete sequence.
1.9e-77:406:96
AC005859
- 10 R-PLACE1003772
Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.
2.2e-29:454:70
AL020997
- 15 R-PLACE1003839
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12, complete sequence.
3.0e-52:272:97
AC004131
- 20 R-PLACE1003845
HS_3219_A1_A10_MRCIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=19 Row=A, genomic survey sequence.
1.5e-13:231:70
AQ181482
- 25 R-PLACE1003852
Homo sapiens mRNA for KIAA0758 protein, partial cds.
6.8e-86:439:96
AB018301
- 30 R-PLACE1004028
- R-PLACE1004078
Homo sapiens 12p13.3 PAC RPCI5-940J5 (Roswell Park Cancer Institute Human PAC Library) complete sequence.
35 5.0e-36:310:80
AC006064
- R-PLACE1004166
40 Petromyzon marinus neurofilament subunit NF-180 mRNA, complete cds.
0.95:224:62
U19361
- R-nnnnnnnnnnnnn
45 Fugu rubripes GSS sequence, clone 076D01bH10, genomic survey sequence.
3.0e-08:107:77
AL026605
- R-PLACE1004199
50 Human prostaglandin D2 synthase gene, exons 2 through 6 and complete cds.
0.0028:157:67
M98538
- R-PLACE1004279
55 Human DNA sequence from PAC 193B12 on chromosome 6p21.3-22.3. Contains histone H2A/d, H2B/d, H2A.i, H1.5, H3.F, H4.k, H3/j genes, histone pH2b.i and hypothetical protein A4 pseudogenes, histone H2A.1 and H2B.2 duplicate genes, Glycine (GGC) tRNA gene, olfactory receptor OL1 like gene, ESTs STSs and predicted CpG islands.

0.00065:228:58
Z98744

R-PLACE1004282

5

R-PLACE1004305
Homo sapiens mRNA for KIAA0740 protein, complete cds.
2.0e-77:377:99
AB018283

10

R-PLACE1004441
RPC111-76P13.TV RPC111 Homo sapiens genomic clone R-76P13, genomic survey sequence.
1.8e-73:370:97
AQ281810

15

R-PLACE1004450
Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence.
0.87:269:59
AB012242

20

R-PLACE1004482
Mus musculus hematopoietic lineage switch 2 (HLS2) mRNA, complete cds.
5.2e-33:356:75
AF009513

25

R-PLACE1004492
Mus musculus mRNA for Doc2, partial cds.
4.1e-28:268:77
D50000

30

R-PLACE1004519
Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence.
1.8e-14:330:67
AL021808

35

R-PLACE1004520
Human pregnancy specific beta-1-glycoprotein 1 (PSG1) gene.
1.4e-73:397:93
M93705

40

R-PLACE1004630

45

R-PLACE1004637
Human Chromosome 11 Cosmid cSRL16b6, complete sequence.
5.5e-108:625:91
U73638

50

R-PLACE1004648

R-PLACE1004816
Homo sapiens mRNA for Hakata antigen, complete cds.
5.6e-103:586:90
D88587

55

R-PLACE1004887
CIT-HSP-2172H20.TR CIT-HSP Homo sapiens genomic clone 2172H20, genomic survey sequence.

- 1.2e-31:177:97
B99962
- 5 R-PLACE1005003
Mus musculus clone OST13719, genomic survey sequence.
0.0043:159:64
AF046703
- 10 R-PLACE1005005
Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds.
2.1e-56:299:95
AF032456
- 15 R-PLACE1005031
Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.
1.0:155:65
AC005821
- 20 R-PLACE1005239
Homo sapiens mRNA for HIRIP3 protein (clone pH4-31, pH4-17).
4.4e-85:450:93
AJ223351
- 25 R-PLACE1005250
Mus musculus maternal transcript Maid (Maid) mRNA, complete cds.
7.7e-19:232:73
U50734
- 30 R-PLACE1005383
Homo sapiens UP50 mRNA, complete cds.
2.0e-77:471:88
AF093118
- 35 R-PLACE1005410
Canis familiaris sec61 homologue mRNA, complete cds.
6.4e-12:132:82
M96629
- 40 R-PLACE1005426
Human pregnancy specific beta-1-glycoprotein 4 (PSG4) mRNA, complete cds.
2.3e-109:574:94
M94891
- 45 R-PLACE1005519
Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SE-
QUENCE.
4.1e-08:426:61
AL034557
- 50 R-PLACE1005539
- R-PLACE1005544
Homo sapiens chromosome 19, cosmid F20887, complete sequence.
1.0e-17:202:73
- 55 AC005578
- R-PLACE1005569
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.

3.8e-89:470:95
AL034397

R-PLACE 1005601

Homo Sapiens angiotensin II receptor gene, complete cds.
8.0e-52:301:90
L48211

R-PLACE1005660

R-PLACE1005669

Mitochondrion Culex torrentium A+T rich mitochondrial control region.
9.5e-09:338:63
U69573

R-PLACE1005682

Caenorhabditis elegans cosmid M70.
0.012:226:62
AF047661

R-PLACE1005725

Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y48E1, WORKING DRAFT SE-
QUENCE.
0.42:435:59
Z92856

R-PLACE1005736

Rattus norvegicus DD6A4-1 mRNA, partial sequence.
9.0e-21:282:73
AF034237

R-PLACE1005745

RPC111-88L20.TJ RPC111 Homo sapiens genomic clone R-88L20, genomic survey sequence.
2.4e-62:310:99
AQ281511

R-PLACE1005768

Human DNA sequence from Fosmid 24E5 on chromosome 22q11.2-qter contains parvalbumin, ESTs, STS.
5.6e-94:511:93
Z82185

R-PLACE1005815

Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.
9.0e-55:586:73
AC002310

R-PLACE1005878

R-PLACE1005927

R-PLACE1006071

CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.
1.6e-76:410:95
AQ022149

R-PLACE1006073

Homo sapiens mRNA for glucuronyltransferase I, complete cds.
2.2e-97:513:93

AB009598

R-PLACE1006079

Homo sapiens distal-less homeobox protein (DLX3) gene, complete cds.

5.4e-57:333:91

AF028233

R-PLACE1006093

R-nnnnnnnnnnnnn

Caenorhabditis elegans mRNA for GAP-2-7, partial cds.

1.9e-08:251:60

AB011283

R-PLACE1006219

HS_3219_A1_A10_MRCIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219

Col=19 Row=A, genomic survey sequence.

3.1e-12:228:69

AQ181482

R-PLACE1006277

Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.

7.8e-96:557:91

AL034397

R-PLACE1006290

Bacillus whitei clone pWH/Cugl satellite DNA.

0.37:209:62

U90159

R-PLACE1006443

Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.

8.9e-76:451:91

AC002093

R-PLACE1006515

Homo sapiens mRNA for KIAA0576 protein, partial cds.

2.1e-76:413:94

AB011148

R-PLACE1006716

M.musculus gene encoding prostaglandin D synthase, putative.

1.0:199:59

Y10138

R-PLACE1006786

HS_2037_A2_B06_MRCIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037

Col=12 Row=C, genomic survey sequence.

0.33:47:91

AQ232754

R-PLACE1006809

Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq28lu2 gene.

0.67:241:59

U52112

- R-PLACE1006959
- R-PLACE1007028
- 5 R-PLACE1007040
Rabbit angiotensin-converting enzyme (ACE-P) gene, 5' end.
0.0037:208:65
M58579
- 10 R-PLACE1007077
CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.
3.0e-76:411:94
AQ022149
- 15 R-PLACE1007081
RPCI11-31D7.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-31D7, genomic survey sequence.
1.9e-06:88:84
AQ016433
- 20 R-PLACE1007096
H.sapiens DMD gene microsatellite (147-200bp).
1.0:142:59
X77677
- 25 R-PLACE1007296
- R-PLACE1007591
Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.
- 30 1.6e-11:203:66
AL023574
- R-PLACE1007626
Homo sapiens unknown mRNA, complete cds.
- 35 4.9e-29:183:91
AF047439
- R-PLACE1007702
Homo sapiens chromosome 17, clone 363G12, WORKING DRAFT SEQUENCE, 11 unordered pieces.
- 40 2.3e-75:445:90
AC002348
- R-PLACE1007845
CIT-HSP-2306G15.TR CIT-HSP Homo sapiens genomic clone 2306G15, genomic survey sequence.
- 45 0.00045:194:64
AQ022229
- R-PLACE1007881
CITBI-E1-2503C21.TF CITBI-E1 Homo sapiens genomic clone 2503C21, genomic survey sequence.
- 50 0.43:104:69
AQ263355
- R-PLACE1007971
- 55 R-PLACE1008282
Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.
7.7e-73:396:94
AC005995

- 5 R-PLACE1008297
N.frontalis enolase gene, promotor region.
1.2e-08:457:57
X81451
- 10 R-PLACE1008359
Plasmodium falciparum MAL3P1, complete sequence.
0.00044:443:56
Z97348
- 15 R-PLACE1008469
Homo sapiens chromosome 17, clone HCIT145P4, WORKING DRAFT SEQUENCE, 8 unordered pieces.
4.4e-78:536:84
AC002093
- 20 R-PLACE1008549
Mus musculus E74-like factor 5 (Elf5) mRNA, complete cds.
3.4e-30:256:75
AF049702
- 25 R-PLACE1008657
Homo sapiens BAC clone GS067A24 from 7q21.q21.2, complete sequence.
1.9e-40:320:82
AC005009
- 30 R-PLACE1008716
Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.
8.2e-118:591:96
U15128
- 35 R-PLACE1008744
Sequence 1 from patent US 5691147.
3.le-108:559:94
I76197
- 40 R-PLACE1008984
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SE-
QUENCE.
1.6e-102:503:96
AL031427
- 45 R-PLACE1008985
Mus musculus synaptotagmin VIII mRNA, partial cds.
9.7e-29:255:77
U20107
- R-PLACE1009067
- 50 R-PLACE1009196
Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y48A6, WORKING DRAFT SE-
QUENCE.
0.0094:206:65
Z92854
- 55 R-PLACE1009279
Homo sapiens serine protease (PRSS11) mRNA, partial cds.
2.4e-26:553:62
AF097709

- 5 R-PLACE1009527
Human DNA-binding protein ABP/ZF mRNA, complete cds.
7.9e-91:497:91
U82613
- 10 R-PLACE1009546
Human PAC clone DJ218B13 from Xq23, complete sequence.
0.29:147:64
AC002072
- 15 R-PLACE1009600
Mouse mRNA for tetracycline transporter-like protein, complete cds.
6.1e-81:466:90
D88315
- 20 R-PLACE1009735
Homo sapiens clone NH0523H20, complete sequence.
2.0e-74:268:99
AC005041
- 25 R-nnnnnnnnnnnnn
Homo sapiens DNA sequence from PAC 833B2 on chromosome Xq26.1-27.2. Contains an EST, complete se-
quence.
1.9e-05:255:65
AL023800
- 30 R-PLACE1010011
, complete sequence.
2.9e-77:174:100
AC005409
- 35 R-PLACE1010078
Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 209H1, WORKING DRAFT SEQUENCE.
1.0:108:65
Z84465
- 40 R-PLACE1010081
Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.
9.2e-105:560:93
AF027706
- 45 R-PLACE1010251
Plasmodium falciparum MAL3P4, complete sequence.
5.0e-07:468:58
AL008970
- 50 R-PLACE1010445
Pan troglodytes HS19.8-similar locus and Y Alu element, genomic survey sequence.
1.2e-49:303:90
AF077058
- 55 R-PLACE1010713
RPC111-69F22.TK RPC111 Homo sapiens genomic clone R-69F22, genomic survey sequence.
7.4e-11:114:80
AQ238297
- R-PLACE1010784
Capra hircus strain Saanen, genomic survey sequence.

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7.4e-24:182:87
AF083406

5 R-PLACE1010827
nbxb0026K23f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0026K23f, genomic survey sequence.
1.0:252:61
AQ271546

10 R-PLACE1010968
Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5
unordered pieces.
0.0038:295:57
AC005308

15 R-PLACE1011045
Homo sapiens E1-like protein mRNA, complete cds.
1.6e-90:453:96
AF094516

20 R-PLACE1011116
Homo sapiens embryonic lung protein (HUEL) mRNA, complete cds.
4.6e-72:385:94
AF006621

25 R-PLACE1011236
*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0289H06; HTGS phase 1,
WORKING DRAFT SEQUENCE, 4 unordered pieces.
0.98:142:65
AC004580

30 R-PLACE1011364

R-PLACE1011407
Human DNA sequence from clone 127F18 on chromosome Xp11.4-21.3. Contains part of a novel gene with some
35 similarity to parts of chicken Myosin Light Chain and various species' Interleukin-1 Receptor Type 1 (IL1-R-1).
Contains GSSs, complete sequence.
9.1e-27:293:74
AL031575

40 R-PLACE1011516
Fugu rubripes GSS sequence, clone 190N14aC12, genomic survey sequence.
1.0:96:68
AL030602

45 R-PLACE1011708
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.
2.4e-91:521:91
AF034611

50 R-PLACE1011824
Figure 6. DNA sequence of three 3'apoB VNTR alleles.
2.2e-06:264:65
M23046

55 R-PLACE1011978
Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.
4.8e-50:553:69
M27877

- 5 R-PLACE2000118
Homo sapiens DNA sequence from PAC 393P12 on chromosome Xp11.21. Contains a hypothetical protein KIAA0413 (KIAA0412, KIAA0065, KIAA0569) LIKE Zinc Finger protein pseudogene, a hypothetical Proline-rich protein KIAA0269 LIKE gene and a 60S Ribosomal Protein L7 LIKE pseudogene. Contains ESTs, an STS and a GSS (BAC end sequence), complete sequence.
3.9e-107:567:94
AL022578
- 10 R-PLACE2000219
Homo sapiens clone RG132J19, complete sequence.
4.7e-39:317:82
AC005163
- 15 R-PLACE3000181
Human protocadherin 42 mRNA, 3' end of cds for alternative splicing PC42-8.
3.9e-81:441:94
L11369
- 20 R-PLACE3000213
Sequence 1 from patent US 5691147.
1.5e-109:559:95
I76197
- 25 R-PLACE4000354
Sequence 1 from patent US 5691147.
2.7e-106:548:95
I76197
- 30 R-PLACE4000455
Arabidopsis thaliana genomic DNA chromosome 3, P1 clone: MEBS, complete sequence.
9.3e-07:357:60
AB019230
- 35 R-THYRO1000036
Sequence 11 from patent US 5773248.
4.0e-99:527:93
AR014074
- 40 R-THYRO1000061
Homo sapiens chromosome 19, cosmid R34382, complete sequence.
7.3e-90:460:96
AC005329
- 45 R-THYRO1000099
- 50 R-THYRO1000196
Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds.
1.1e-104:530:96
AF016272
- 55 R-THYRO1000400
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-233A8, complete sequence.
1.0:308:61
AC004685
- R-THYRO1000580
Human Kox26 mRNA for zinc finger protein, partial.
0.11:105:67

- X52357
- R-THYRO1000584
 *** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0539L10; HTGS phase 1,
 5 WORKING DRAFT SEQUENCE, 15 unordered pieces.
 1.4e-14:241:68
 AC004480
- R-THYRO1000678
 10 Belonogaster petiolata 16S ribosomal RNA gene, mitochondrial gene for mitochondrial rRNA, partial sequence.
 0.049:150:64
 AF066910
- R-THYRO1000776
 15 CITBI-E1-2505N5.TF.1 CITBI-E1 Homo sapiens genomic clone 2505N5, genomic survey sequence.
 0.38:179:63
 AQ241670
- R-THYRO1000795
 20 R-THYRO1000846
 Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, complete cds.
 3.6e-06:425:61
 AF029779
- R-THYRO1000866
 25 Homo sapiens SKB1Hs mRNA, complete cds.
 4.0e-42:251:92
 AF015913
- R-THYRO1000956
 30 R-THYRO1000964
 Human Chromosome 11 Cosmid cSRL186g7, complete sequence.
 35 0.18:292:61
 U73627
- R-THYRO1000999
 40 CIT-HSP-2288E24.TR CIT-HSP Homo sapiens genomic clone 2288E24, genomic survey sequence.
 3.6e-18:292:71
 AQ002356
- R-THYRO1001063
 45 Homo sapiens chromosome 16 BAC clone CIT987SK-381E11 complete sequence.
 1.5e-27:292:76
 AF001552
- R-THYRO1001071
 50 Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 37E16, WORKING DRAFT SEQUENCE.
 1.7e-105:513:98
 Z83844
- R-THYRO1001102
 55 Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.
 3.2e-62:429:86
 AC004832
- R-THYRO1001113

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Caenorhabditis elegans cosmid C25F9, complete sequence.

0.026:338:58

Z81476

5

R-THYRO1001128

Homo sapiens chromosome 9q34, clone 63G10, complete sequence.

5.3e-12:132:79

AC002096

10

R-THYRO1001205

Homo sapiens clone DJ1173I20, WORKING DRAFT SEQUENCE, 5 unordered pieces.

1.9e-60:251:85

AC004987

15

R-THYRO1001237

R-THYRO1001242

Mouse mRNA for thymic epithelial cell surface antigen, complete cds.

1.5e-45:525:75

20

D67067

R-THYRO1001266

H.sapiens DNA containing a polymorphic (CA)_n repeat (436bp).

6.0e-05:258:67

25

X65457

R-THYRO1001327

Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.

2.8e-104:541:95

30

AL021578

R-THYRO1001456

35

R-THYRO1001457

H.sapiens mRNA for protein kinase C mu.

2.9e-23:391:66

X75756

40

R-THYRO1001471

Homo sapiens Chromosome 16 BAC clone CIT987SK-A-952F10, complete sequence.

0.39:271:61

AC004787

45

R-THYRO1001478

R-THYRO1001495

Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces.

2.8e-88:446:88

50

AC006006

R-THYRO1001523

CIT-HSP-2333F9.TF CIT-HSP Homo sapiens genomic clone 2333F9, genomic survey sequence.

1.4e-05:126:71

55

AQ039390

R-THYRO1001529

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- 5 R-THYRO1001593
Homo sapiens chromosome 19, cosmid R33632, complete sequence.
3.7e-100:514:96
AC005781
- 10 R-THYRO1001608
Homo sapiens clone DJ0635005, WORKING DRAFT SEQUENCE, 7 unordered pieces.
2.3e-40:369:79
AC004845
- 15 R-THYRO1001641
Homo sapiens clone 24448 unknown mRNA, partial cds.
3.4e-110:562:96
AF070638
- 20 R-THYRO1001700
- R-THYRO1001702
Mus musculus mRNA for myeloid associated differentiation protein.
1.1e-11:367:66
AJ001616
- 25 R-THYRO1001725
Homo sapiens, clone hRPK.1_A_1, complete sequence.
9.1e-12:329:65
AC006196
- 30 R-THYRO1001770
Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence.
0.12:339:59
AC004879
- R-THYRO1001803
- 35 R-Y79AA1000030
Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.
2.0e-98:515:95
AC005214
- 40 R-Y79AA1000127
Homo sapiens genomic DNA, chromosome 21q11.1, segment 5/28, WORKING DRAFT SEQUENCE.
3.2e-115:551:99
AP000034
- 45 R-Y79AA1000207
Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.
1.8e-38:282:85
AC005562
- 50 R-Y79AA1000226
Homo sapiens full length insert cDNA YN52F10.
4.8e-09:104:85
AF075033
- 55 R-Y79AA1000270
Human mRNA for ORF, Xq terminal portion.
1.0e-105:564:93
D16469

- 5 R-Y79AA1000426
Rattus norvegicus activin beta E mRNA, complete cds.
6.1e-50:562:72
AF089825
- 10 R-Y79AA1000521
Rattus norvegicus steroid sulfatase (Sts) mRNA, complete cds.
0.48:233:62
U37138
- 15 R-Y79AA1000750
Human DNA from cosmid f23280 from chromosome 19q13.2, genomic sequence.
6.8e-07:320:60
L47334
- 20 R-Y79AA1000776
R-Y79AA1000777
Homo sapiens full length insert cDNA clone ZD93D10.
2.9e-110:574:95
AF088072
- 25 R-Y79AA1000876
Mus musculus bone morphogenetic protein-6 (BMP-6) gene, exons 6 and 7 and complete cds.
0.0096:105:71
U73520
- 30 R-Y79AA1000959
Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds.
1.0e-78:453:92
AF093420
- 35 R-Y79AA1000967
Rattus norvegicus vesicle-associate calmodulin-binding protein mRNA, complete cds.
2.3e-43:263:84
L22557
- 40 R-Y79AA1001013
R-Y79AA1001056
Mus musculus maternal transcript Maid (Maid) mRNA, complete cds.
1.5e-22:269:73
U50734
- 45 R-Y79AA1001062
D.teissieri mitochondrial DNA for tRNA-Ile, tRNA-Gln & tRNA-Val.
1.1e-07:494:57
X54011
- 50 R-Y79AA1001090
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.
1.2e-26:269:77
AC002300
- 55 R-Y79AA1001212
Homo sapiens SL15 protein mRNA, complete cds.
5.7e-82:407:97
AF038961

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- R-Y79AA1001264
HS_2195_A2_A07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195
Col=14 Row=A, genomic survey sequence.
3.4e-07:101:82
5 AQ191092
- R-Y79AA1001272
Hansenula wingei mitochondrial DNA, complete sequence.
2.1e-05:435:60
10 D31785
- R-Y79AA1001328
Rattus norvegicus Delta 3 mRNA, complete cds.
1.0e-29:356:72
15 AF084576
- R-Y79AA1001426
- R-Y79AA1001430
20 Homo sapiens mRNA for KIAA0469 protein, complete cds.
6.2e-111:555:96
AB007938
- R-Y79AA1001523
25 Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8
(Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete
sequence.
3.7e-71:259:90
Z84480
30
- R-Y79AA1001530
Human beta-tubulin gene (5-beta) with ten Alu family members.
2.6e-56:301:96
X00734
35
- R-Y79AA1001592
HS_2175_A2_B11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2175
Col=22 Row=C, genomic survey sequence.
1.0:237:59
40 AQ307634
- R-Y79AA1001727
- R-Y79AA1001787
45 Homo sapiens mRNA for putative ATPase, partial.
7.2e-80:405:97
AJ009947
- R-Y79AA1001795
50 Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the BINGS gene, exons 11
to 15 of the BING4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein
S18) gene, the SACM2L (suppressor of actin mutation 2, yeast, homolog) gene, a pseudogene similar to TAT-
SF1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6 (RING2), the gene for HKE4
(RING5), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen, type XI, alpha 2) gene, the HLA-
55 DPB2 pseudogene and part of the HLA-DPA3 pseudogene. Contains predicted CpG islands, ESTs, STSs, and
GSSs, complete sequence.
4.2e-110:555:97
AL031228

- R-Y79AA1001799
- R-Y79AA1001803
 Rattus norvegicus secretogranin III (SgIII) mRNA, complete cds.
 5 6.2e-60:499:77
 U02983
- R-Y79AA1001863
 Human DNA sequence from PAC 365E2 on chromosome 6p22.3-24.1. Contains EST and STS.
 10 1.4e-45:261:75
 AL009177
- R-Y79AA1002022
 H.sapiens mRNA for basement membrane heparan sulfate proteoglycan.
 15 1.0:311:61
 X62515
- R-nnnnnnnnnnnnn
 Plasmodium falciparum chromosome 2, section 18 of 73 of the complete sequence.
 20 1.0:208:62
 AE001381
- R-nnnnnnnnnnnnn
 Homo sapiens DNA, trinucleotide repeats region, clone CAG83.
 25 0.17:132:67
 AB018494
- R-Y79AA1002213
 Human DNA sequence from PAC 340G1 on chromosome 6 contains STS.
 30 5.6e-46:490:73
 Z84719
- R-Y79AA1002334
 Japanese Quail (C.coturnix) troponin T isoform mRNA, clone cC501.
 35 0.96:210:63
 M26599
- R-Y79AA1002373
 Human BAC clone RG126M09 from 7q21-q22, complete sequence.
 40 9.7e-82:544:85
 AC002067
- R-Y79AA1002376
 Human mitochondrial DNA, fragment M1, encoding transfer RNAs, cytochrome oxidase I, and 2 URFs.
 45 1.9e-111:546:97
 M10546
- R-Y79AA1002378
 Mus musculus mRNA for zinc finger protein, complete cds, clone:CTfin51.
 50 1.5e-33:244:74
 D10630
- R-Y79AA1002381
 Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK
 55 p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK
 p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.
 0.0046:177:68
 Z95152

Homology search result 8.

[0300] The result of the homology search in the Human Unigene(<http://www.ncbi.nlm.nih.gov/UniGene>) using the clone sequences of the 5'-ends.

5

Indicated are from the top,
the name of the clone sequence,
title of the top hit data,
the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
the Accession No. of the top hit data.

10

[0301] Data were not shown for the clones in which the P-value was higher than 1.

15

F-BNGH41000020
ESTs
6.6e-72:412:92
Hs.153375:AI287812

20

F-BNGH41000087
Homo sapiens mRNA for MIFR-1, complete cds
0.027:499:57
Hs.58269:AB010962

25

F-BNGH41000091
Homo sapiens voltage-gated potassium channel eag (EAG) mRNA, complete cds
5.2e-81:687:76
Hs.158305:AJ001366

30

F-HEMBA1000006
ESTs, Weakly similar to HYPOTHETICAL 51.2 KD PROTEIN IN LAG1-RPL14B INTERGENIC REGION [S.cerevisiae]
2.0e-25:167:91
Hs.9252:R53360

35

F-HEMBA1000121
ESTs, Moderately similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]
3.0e-34:180:98
Hs.149509:N24022

40

F-HEMBA1000128
EST
0.00069:177:62
Hs.158854:AI377837

45

F-HEMBA1000275
Human modulator recognition factor I (MRF-1) mRNA, 3'end
0.012:508:58
Hs.920:M62324

50

F-HEMBA1000300
Human mRNA for KIAA0355 gene, complete cds
1.6e-46:402:78
Hs.153014:AB002353

55

F-HEMBA1000349
EST
6.7e-08:65:95

- Hs.54372:N80032
- F-HEMBA1000443
ESTs
5 6.1e-23:278:76
Hs.69492:AA116026
- F-HEMBA1000462
- 10 F-HEMBA1000477
ESTs
6.9e-78:414:94
Hs.152861:AA287444
- 15 F-HEMBA1000590
Homo sapiens mRNA for matrilin-4, partial
7.3e-95:482:96
Hs.129361:AJ007581
- 20 F-HEMBA1000634
ESTs
1.3e-38:246:86
Hs.6145:W26640
- 25 F-HEMBA1000671
Zinc finger protein 140 (clone pHZ-39)
2.4e-53:469:68
Hs.154205:U09368
- 30 F-HEMBA1000713
Homo sapiens 10kD protein (BC10) mRNA, complete cds
2.1e-127:442:97
Hs.5300:AF053470
- 35 F-HEMBA1000732
Homo sapiens latent transforming growth factor-beta binding protein 4S mRNA, complete cds
1.0e-45:258:94
Hs.85087:AF051344
- 40 F-HEMBA1000745
Human cardiotrophin-1 (CTF1) mRNA, complete cds
1.1e-07:316:61
Hs.25537:U43030
- 45 F-HEMBA1000835
ESTs
4.2e-11:188:72
Hs.116265:AI184988
- 50 F-HEMBA1000875
Zinc finger protein 133 (clone pHZ-13)
1.5e-27:169:93
Hs.78434:U09366
- 55 F-HEMBA1000907
Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds
1.3e-06:545:60
Hs.143551:AF048693

- 5 F-HEMBA1000940
Homo sapiens connexin46.6 (Cx46.6) gene, complete cds
4.1e-18:307:66
Hs.100072:AF014643
- 10 F-HEMBA1000962
Homo sapiens mRNA for MEGF8, partial cds
0.0018:391:62
Hs.158200:AB011541
- 15 F-HEMBA1001184
Homo sapiens SH3 domain binding glutamic acid-rich-like protein (SH3BGRL) mRNA, complete cds
2.7e-24:404:67
Hs.14368:AF042081
- 20 F-HEMBA1001221
Human transmembrane protein mRNA, complete cds
7.7e-44:858:63
Hs.78531:U19878
- 25 F-HEMBA1001228
Human germline oligomeric matrix protein (COMP) mRNA, complete cds
2.2e-85:463:93
Hs.1584:AC003107
- 30 F-HEMBA1001272
Antidiuretic hormone receptor
0.064:616:57
Hs.2524:L22206
- 35 F-HEMBA1001296
Homo sapiens delta-catenin mRNA, complete cds
0.031:410:59
Hs.80220:U96136
- 40 F-HEMBA1001297
Homo sapiens putative transcription factor CA150 mRNA, complete cds
3.0e-15:143:81
Hs.13063:AF017789
- 45 F-HEMBA1001390
ESTs, Highly similar to polymerase I-transcript release factor [M.musculus]
1.6e-49:297:91
Hs.25581:AI246284
- 50 F-HEMBA1001563
ESTs
4.9e-12:160:74
Hs.162813:AA524616
- 55 F-HEMBA1001621
Human P2U nucleotide receptor mRNA, complete cds
0.00098:314:61
Hs.339:U07225
- F-HEMBA1001878
Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds
3.4e-172:810:98

Hs.10290:AF090988

F-HEMBA1001886
Human repressor transcriptional factor (ZNF85) mRNA, complete cds
5 1.1e-115:849:80
Hs.37138:U35376

F-HEMBA1002048
Homo sapiens mRNA for APC 2 protein, complete cds
10 0.96:266:62
Hs.20912:AB012162

F-HEMBA1002131
Homo sapiens mRNA for KIAA0584 protein, partial cds
15 1.1e-45:709:66
Hs.106794:AB011156

F-HEMBA1002163
ASPARTYL-TRNA SYNTHETASE
20 0.026:568:58
Hs.80758:J05032

F-HEMBA1002164
Pregnancy-associated plasma protein A
25 0.0049:274:60
Hs.158229:U28727

F-HEMBA1002167

30 F-HEMBA1002178
Homo sapiens mRNA for KIAA0584 protein, partial cds
8.3e-48:794:65
Hs.106794:AB011156

35 F-HEMBA1002195
EST
2.0e-05:177:70
Hs.145935:AI275921

40 F-HEMBA1002227
Myristoylated alanine-rich C-kinase substrate
1.2e-138:382:95
Hs.75607:D10522

45 F-HEMBA1002239
Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488
1.2e-47:570:71
Hs.67619:AB007957

50 F-HEMBA1002316
EST
1.8e-28:246:79
Hs.136950:AA825638

55 F-HEMBA1002420
Homo sapiens GABA-B receptor mRNA, complete cds
1.7e-05:303:63
Hs.12307:AF056085

- 5 F-HEMBA1002421
Syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)
4.3e-167:778:98
Hs.1501:J04621
- 10 F-HEMBA1002524
Human MHC Class I region proline rich protein mRNA, complete cds
8.5e-128:751:89
Hs.41548:U63336
- 15 F-HEMBA1002551
ESTs
2.4e-25:207:84
Hs.158172:N24325
- 20 F-HEMBA1002767
Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds
4.4e-170:798:98
Hs.19154:AF038660
- 25 F-HEMBA1002985
ESTs
2.6e-09:124:76
Hs.118620:T60326
- 30 F-HEMBA1002992
ESTs
2.4e-21:121:97
Hs.143571:AI089396
- 35 F-HEMBA1003047
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds
1.5e-188:873:99
Hs.148318:AF034611
- 40 F-HEMBA1003072
ESTs
1.2e-33:387:71
Hs.59628:W91959
- 45 F-HEMBA1003101
Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds
1.7e-140:671:98
Hs.26350:AF049891
- 50 F-HEMBA1003120
Zinc finger protein 91 (HPF7, HTF10)
1.0e-24:143:76
Hs.8597:L11672
- 55 F-HEMBA1003230
Homo sapiens UP50 mRNA, complete cds
1.8e-184:856:98
Hs.11494:AF093118
- F-HEMBA1003294
Human antiseecretory factor-1 mRNA, complete cds
5.1e-45:324:83

Hs.148495:AF050199

F-HEMBA1003315
Homo sapiens mRNA for TIP49, complete cds
5 4.2e-19:377:64
Hs.155541:AF070735

F-HEMBA1003392
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds
10 9.2e-185:851:99
Hs.23672:AF074264

F-HEMBA1003399
H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase
15 0.00042:297:61
Hs.118929:X79568

F-HEMBA1003487
Homo sapiens receptor for viral semaphorin protein (VESPR) mRNA, complete cds
20 0.0011:237:63
Hs.88145:AF030339

F-HEMBA1003497
ESTs, Weakly similar to similar to zinc finger 5 protein from Gallus gallus, U51640 [H.sapiens]
25 2.5e-09:303:63
Hs.143723:H86048

F-HEMBA1003530
Homo sapiens mRNA for ephrin-A2
30 0.024:396:60
Hs.158306:AJ007292

F-HEMBA1003602
Homo sapiens DNA from chromosome 19, cosmid R29144
35 0.0072:663:57
Hs.155647:AC004221

F-HEMBA1003732
ESTs
40 1.0e-106:494:100
Hs.157568:AI356515

F-HEMBA1003945
Homo sapiens clone 638 unknown nRNA, complete sequence
45 5.9e-78:310:93
Hs.159515:AF091085

F-HEMBA1004007
PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC
50 0.56:165:64
Hs.115742:AF077754

F-HEMBA1004067
Fatty acid synthase {3' region} [human, breast and HepG2 cells, mRNA Partial, 2237 nt]
55 0.048:581:58
Hs.83190:U29344

F-HEMBA1004085

- ESTs
1.7e-15:92:98
Hs.98138:AI183561
- 5 F-HEMBA1004110
Homo sapiens intersectin short form mRNA, complete cds
1.2e-159:779:96
Hs.66392:AF064244
- 10 F-HEMBA1004250
Human mRNA for KIAA0327 protein, complete cds
2.1e-23:676:59
Hs.149323:AB002325
- 15 F-HEMBA1004391
NEURAL CELL ADHESION MOLECULE L1 PRECURSOR
0.43:157:63
Hs.1757:U52112
- 20 F-HEMBA1004444
H.sapiens mRNA for gp25L2 protein
1.5e-54:544:73
Hs.159569:X90872
- 25 F-HEMBA1004454
Homo sapiens tetraspan NET-4 mRNA, complete cds
1.1e-05:230:62
Hs.20709:AF065389
- 30 F-HEMBA1004505
ESTs
9.1e-61:345:93
Hs.4814:AA631254
- 35 F-HEMBA1004785
Homo sapiens Polycomb 2 homolog (hPc2) mRNA, complete cds
3.7e-18:294:65
Hs.123085:AF013956
- 40 F-HEMBA1004797
ESTs
3.9e-06:107:73
Hs.42302:AI032142
- 45 F-HEMBA1004952
Human cardiotrophin-1 (CTF1) mRNA, complete cds
0.00021:175:68
Hs.25537:U43030
- 50 F-HEMBA1004971

F-HEMBA1004982
Human metabotropic glutamate receptor 8 mRNA, complete cds
0.31:288:60
- 55 Hs.86204:U92459

F-HEMBA1005070
Human mRNA for KIAA0310 gene, complete cds

- 7.9e-67:370:93
Hs.5716:AB002308
- 5 F-HEMBA1005084
Homo sapiens mRNA for KIAA0612 protein, partial cds
0.00022:400:59
Hs.112499:AB014512
- 10 F-HEMBA1005145
Lymphocyte-activation gene 3
3.4e-05:480:59
Hs.74011:X51985
- 15 F-HEMBA1005230
ESTs
2.3e-103:481:99
Hs.135112:AI090827
- 20 F-HEMBA1005246
Homo sapiens ALR mRNA, complete cds
2.0e-05:220:62
Hs.153638:AF010403
- 25 F-HEMBA1005267
ESTs
5.6e-16:305:64
Hs.125699:AA868017
- 30 F-HEMBA1005337
EST
2.1e-59:304:97
Hs.48956:N64339
- 35 F-HEMBA1005430
ESTs
6.9e-19:333:65
Hs.116567:AI332643
- 40 F-HEMBA1005449
Human plectin (PLEC1) mRNA, complete cds
0.026:576:56
Hs.79706:U53204
- 45 F-HEMBA1005489
Homo sapiens mRNA for KIAA0291 gene, partial cds
0.14:551:59
Hs.104717:AB006629
- 50 F-HEMBA1005522
COAGULATION FACTOR VII PRECURSOR
1.8e-12:298:64
Hs.36989:M13232
- 55 F-HEMBA1005545
MUSCARINIC ACETYLCHOLINE RECEPTOR M3
2.6e-143:672:98
Hs.7138:U29589

- 5 F-HEMBA1005698
ESTs
1.8e-124:611:97
Hs.144441:AI338335
- F-HEMBA1005913
- 10 F-HEMBA1005929
H.sapiens mRNA for serine/threonine protein kinase EMK
1.5e-86:847:72
Hs.157199:X97630
- 15 F-HEMBA1005945
ESTs, Weakly similar to F17E5.2 [C.elegans]
4.2e-26:159:92
Hs.126571:AI038963
- 20 F-HEMBA1006016
ESTs
1.3e-22:145:93
Hs.33728:H97503
- F-HEMBA1006171
- 25 F-HEMBA1006276
Homo sapiens KIAA0412 mRNA, partial cds
5.1e-19:371:65
Hs.6200:AB007872
- 30 F-HEMBA1006299
- F-HEMBA1006311
- 35 F-HEMBA1006335
ESTs
0.00021:327:62
Hs.146044:AI089998
- 40 F-HEMBA1006357
Homo sapiens secretory carrier membrane protein (SCAMP2) mRNA, complete cds
7.4e-28:389:67
Hs.10761:AF005038
- 45 F-HEMBA1006430
ESTs
9.7e-92:463:95
Hs.143702:AI084062
- 50 F-HEMBA1006482
Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds
6.2e-146:575:98
Hs.14511:AF026852
- 55 F-HEMBA1006517
ESTs
3.6e-63:381:87
Hs.11611:W21919

5 F-HEMBA1006544
Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds
2.0e-50:503:76
Hs.43543:AF042800

10 F-HEMBA1006572
Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
0.031:611:57
Hs.96253:U79666

15 F-HEMBA1006658
Homo sapiens mRNA for KIAA0687 protein, partial cds
1.2e-128:646:95
Hs.3628:AB014587

20 F-HEMBA1006707
Homo sapiens mRNA for matrilin-4, partial
1.7e-101:476:98
Hs.129361:AJ007581

25 F-HEMBA1006724
ESTs
8.3e-86:450:95
Hs.10056:AA210796

30 F-HEMBA1006749
Homo sapiens mRNA for matrilin-4, partial
6.1e-97:457:98
Hs.129361:AJ007581

35 F-HEMBA1006770
ESTs, Highly similar to BRAIN PROTEIN F41 [Mus musculus]
1.6e-31:237:85
Hs.31612:H41366

40 F-HEMBA1006902
Homo sapiens mRNA for matrilin-4, partial
9.4e-113:541:97
Hs.129361:AJ007581

45 F-HEMBA1006912
ESTs
1.4e-94:460:97
Hs.88672:AA279956

50 F-HEMBA1006916
Homo sapiens Grb14 mRNA, complete cds
5.2e-120:651:92
Hs.83070:L76687

55 F-HEMBA1006960
Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds
0.011:628:57
Hs.159234:U89995

F-HEMBA1007013
ESTs
2.6e-05:139:69

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- Hs.113817:AA702497
- F-HEMBA1007057
Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds
5 7.5e-12:389:64
Hs.143641:AB009462
- F-HEMBA1007063
- 10 F-HEMBA1007226
ESTs
1.8e-35:202:94
Hs.105140:N32669
- 15 F-HEMBA1007241
ESTs, Weakly similar to No definition line found [C.elegans]
4.1e-27:361:67
Hs.114062:AI421699
- 20 F-HEMBA1007291
ESTs
0.96:114:69
Hs.121411:AA770241
- 25 F-HEMBA1007332
ESTs, Weakly similar to hTAFII100 [H.sapiens]
2.5e-81:405:97
Hs.3727:AA205887
- 30 F-HEMBA1000106
ESTs
2.2e-76:393:96
Hs.151874:AI023405
- 35 F-HEMBA1000276
EST
0.81:239:63
Hs.149811:AI286277
- 40 F-HEMBA1000309
Homo sapiens zinc finger protein (MBLL) mRNA, complete cds
2.4e-35:180:100
Hs.44806:AF061261
- 45 F-HEMBA1000407
Cyclin-dependent kinase inhibitor 1C (p57, Kip2)
0.026:218:65
Hs.106070:U22398
- 50 F-HEMBA1000447
Homo sapiens JWA protein mRNA, complete cds
4.6e-160:750:98
Hs.92384:AF070523
- 55 F-HEMBA1000542
ESTs, Weakly similar to C01H6.7 [C.elegans]
6.8e-07:130:77
Hs.18171:AA524327

5 F-HEMBB1000567
ESTs
8.8e-13:271:71
Hs.19934:AA455673

F-HEMBB1000642

10 F-HEMBB1000668
EST
0.83:192:58
Hs.126372:AA912193

F-HEMBB1000679
H.sapiens mRNA for TRAMP protein
15 4.1e-96:727:80
Hs.4147:X63679

F-HEMBB1000881
Homo sapiens chromosome 4p homeobox mRNA sequence
20 2.2e-06:512:60
Hs.104134:M99587

F-HEMBB1000905
Homo sapiens mRNA for voltage gated potassium channel
25 0.93:337:58
Hs.4975:Y15065

F-HEMBB1001026
Human p76 mRNA, complete cds
30 6.1e-08:410:61
Hs.28757:U81006

F-HEMBB1001048
Human Hpast (HPAST) mRNA, complete cds
35 2.1e-56:524:75
Hs.155119:AF001434

F-HEMBB 1001200
EST
40 0.10:300:61
Hs.161647:AA133367

F-HEMBB1001407
Homo sapiens PRKY exon 1 and joined CDS
45 2.6e-40:271:81
Hs.56336:Y15801

F-HEMBB1001530
ESTs
50 1.2e-98:477:98
Hs.135208:AI093908

F-HEMBB1001547

55 F-HEMBB1001573
EST
2.2e-06:115:75
Hs.138275:R43976

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F-HEMBB1001847
 ESTs
 5.3e-79:389:98
 Hs.16141:W56079
 5
 F-HEMBB1001959
 Homo sapiens clone 24781 mRNA sequence
 1.0e-58:322:93
 Hs.108112:AF070640
 10
 F-HEMBB1001978
 EST
 4.7e-23:245:74
 Hs.136356:AA493225
 15
 F-HEMBB1002039
 EST
 2.3e-25:345:70
 Hs.128248:AA972858
 20
 F-HEMBB1002041
 Human plectin (PLEC1) mRNA, complete cds
 2.2e-08:477:60
 Hs.79706:U53204
 25
 F-HEMBB1002051
 Homo sapiens E74-like factor 5 (ELF5) mRNA, complete cds
 9.9e-97:454:99
 Hs.159267:AF049703
 30
 F-HEMBB1002120
 ESTs
 7.6e-10:68:100
 Hs.146335:AI262660
 35
 F-HEMBB1002162
 Homo sapiens genethonin 1 mRNA, complete cds
 2.2e-68:328:99
 Hs.109590:AF062534
 40
 F-HEMBB1002228
 Homo sapiens unknown mRNA, complete cds
 5.3e-41:208:98
 Hs.11441:AF047439
 45
 F-HEMBB1002245
 Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds
 5.6e-05:299:63
 Hs.92614:M62302
 50
 F-HEMBB1002302
 F-HEMBB1002427
 Homo sapiens GN6ST mRNA for long form of N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete
 55
 cds
 0.84:108:68
 Hs.8786:AB014680

- F-HEMBB1002465
ESTs, Highly similar to ACYL-COA DEHYDROGENASE [Bacillus subtilis]
3.2e-18:159:84
Hs.14791:AA741056
- 5 F-HEMBB1002661
ESTs
0.023:424:55
Hs.154029:AI380603
- 10 F-HEMBB1002663
F-HEMBB1002693
- 15 F-MAMMA1000046
Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)
3.2e-43:454:74
Hs.144563:AF057280
- 20 F-MAMMA1000102
Homo sapiens mRNA for cathepsin V, complete cds
0.70:222:65
Hs.87417:AB001928
- 25 F-MAMMA1000106
Homo sapiens mRNA for KIAA0754 protein, partial cds
0.00076:331:61
Hs.159183:AB018297
- 30 F-MAMMA1000118
B94 PROTEIN
1.5e-07:511:61
Hs.75522:M92357
- 35 F-MAMMA1000141
ESTs
2.3e-18:268:73
Hs.155334:AA827904
- 40 F-MAMMA1000204
Homo sapiens dysferlin mRNA, complete cds
2.5e-167:781:98
Hs.143897:AF075575
- 45 F-MAMMA1000226
Human involucrin mRNA
0.0010:414:61
Hs.157091:M13903
- 50 F-MAMMA1000403
ESTs
2.0e-24:163:90
Hs.44281:AI342377
- 55 F-MAMMA1000449
ESTs
0.99:211:60
Hs.143715:AI167929

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F-MAMMA1000457
 NADH-CYTOCHROME B5 REDUCTASE
 7.7e-37:551:66
 Hs.75666:M28713
 5

F-MAMMA1000473
 F-MAMMA1000496
 Homo sapiens PAC clone DJ130H16 from 22q12.1-qter
 1.1e-107:543:96
 Hs.8003:AC004997
 10

F-MAMMA1000528
 EST
 0.22:227:59
 Hs.161400:AI423879
 15

F-MAMMA1000591
 H.sapiens mRNA for UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase
 3.3e-23:470:62
 Hs.55823:X92689
 20

F-MAMMA1000614
 H.sapiens mRNA for CCAAT/enhancer binding protein alpha
 1.9e-06:492:61
 Hs.76171:Y11525
 25

F-MAMMA1000652
 Homo sapiens mRNA, chromosome I specific transcript KIAA0487
 1.5e-61:449:75
 Hs.92381:AB007956
 30

F-MAMMA1000681
 Homo sapiens mRNA for putative G-protein coupled receptor, EDG6
 4.0e-34:636:65
 Hs.159543:AJ000479
 35

F-MAMMA1000706
 COAGULATION FACTOR VII PRECURSOR
 9.7e-16:378:65
 Hs.36989:M13232
 40

F-MAMMA1000788
 ESTs, Weakly similar to M01E11.2 [C.elegans]
 3.4e-118:571:97
 Hs.78389:AI191127
 45

F-MAMMA1000810
 EST
 0.065:211:61
 Hs.116798:AA633813
 50

F-MAMMA1000814
 EST
 3.1e-08:224:66
 Hs.141620:N63316
 55

F-MAMMA1000881

- Homo sapiens sgk gene
3.5e-08:165:69
Hs.159640:AJ000512
- 5 F-MAMMA1000986
Homo sapiens clone 24796 mRNA sequence
2.3e-115:320:99
Hs.27191:AF070596
- 10 F-MAMMA1000994
Human HOX4C mRNA for a homeobox protein
0.050:178:64
Hs.74061:X59372
- 15 F-MAMMA1001043
Latent transforming growth factor beta binding protein 2
0.0013:376:60
Hs.83337:Z37976
- 20 F-MAMMA1001066
ESTs
1.1e-18:128:77
Hs.114031:AA700958
- 25 F-MAMMA1001094
Homo sapiens clone 243 unknown mRNA, complete sequence
2.0e-182:844:99
Hs.20423:AF091094
- 30 F-MAMMA1001141
Homo sapiens achaete scute homologous protein (ASH1) mRNA, complete cds
6.1e-07:492:58
Hs.1619:L08424
- 35 F-MAMMA1001150
Protein kinase C, mu
8.3e-51:691:67
Hs.2891:X75756
- 40 F-MAMMA1001237
Homo sapiens monocarboxylate transporter (MCT3) mRNA, complete cds
8.2e-08:386:60
Hs.85838:U81800
- 45 F-MAMMA1001284
ESTs
1.1e-91:452:97
Hs.114756:AI279440
- 50 F-MAMMA1001310
Homo sapiens mRNA for KIAA0708 protein, partial cds
0.014:512:57
Hs.117177:AB014608
- 55 F-MAMMA1001344
ESTs, Weakly similar to No definition line found [C.elegans]
8.3e-80:406:96
Hs.121619:AI188389

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- 5 F-MAMMA1001418
Human Na⁺/nucleoside cotransporter (hCNT1a) mRNA, complete cds
1.9e-36:622:63
Hs.97207:U62966
- 10 F-MAMMA1001532
Human kruppel-related zinc finger protein (ZNF184) mRNA, partial cds
2.1e-33:282:68
Hs.158174:U66561
- 15 F-MAMMA1001609
Insulin-like growth factor-binding protein 4
0.00026:596:57
Hs.1516:U20982
- 20 F-MAMMA1001615
Homo sapiens DNA from chromosome 19, cosmid R29144
1.1e-05:504:59
Hs.155647:AC004221
- 25 F-MAMMA1001623
Excision repair protein ERCC6
1.2e-38:274:86
Hs.99924:L04791
- 30 F-MAMMA1001634
ESTs
1.5e-26:176:90
Hs.16187:AI139901
- 35 F-MAMMA1001893
Cyclin-dependent kinase inhibitor 1C (p57, Kip2)
0.00030:170:68
Hs.106070:U22398
- 40 F-MAMMA1001901
ESTs
1.5e-36:201:76
Hs.161660:AA167744
- 45 F-MAMMA1001957
Prostaglandin I2 (prostacyclin) receptor (IP)
0.041:277:61
Hs.393:D38128
- 50 F-MAMMA1001978
EST
4.0e-43:359:81
Hs.136494:AA587773
- 55 F-MAMMA1002070
Human PAC clone DJ515N1 from 22q11.2-q22
5.1e-135:652:97
Hs.26670:AC002073
- F-MAMMA1002080
Calcium channel, voltage-dependent, L type, alpha 1C subunit
0.0019:574:57

- Hs.89925:L04569
- F-MAMMA1002087
Human mRNA for KIAA0009 gene, complete cds
5 0.71:228:63
Hs.79972:D13634
- F-MAMMA1002091
Homo sapiens CD39L2 (CD39L2) mRNA, complete cds
10 5.2e-158:743:98
Hs.12330:AF039916
- F-MAMMA1002095
Homo sapiens mRNA for KIAA0703 protein, complete cds
15 4.9e-55:657:68
Hs.6168:AB014603
- F-MAMMA1002128
Human leucine zipper on the D14S46E locus mRNA, complete cds
20 0.77:449:59
Hs.89606:M95925
- F-MAMMA1002142
- F-MAMMA1002165
Homo sapiens connective tissue growth factor-like protein precursor, mRNA, complete cds
25 1.2e-35:182:98
Hs.139340:AF083500
- F-MAMMA1002205
ESTs
30 4.7e-32:385:71
Hs.46158:AI160121
- F-MAMMA1002224
TRANSCRIPTION INITIATION FACTOR IIE, ALPHA SUBUNIT
35 1.3e-34:248:85
Hs.3006:X63468
- F-MAMMA1002234
ESTs
40 1.1e-100:501:97
Hs.158161:AA312511
- F-MAMMA1002586
Human mRNA for KIAA0183 gene, partial cds
45 0.00041:388:61
Hs.76666:D80005
- F-MAMMA1002633
Landsteiner-Wiener blood group glycoprotein
50 1.1e-37:477:71
Hs.108287:L27670
- F-MAMMA1003126
Human Hpast (HPAST) mRNA, complete cds
55 4.1e-84:801:74
Hs.155119:AF001434

- F-NT2RM1000407
ESTs
4.1e-19:132:92
Hs.133484:D80522
- 5 F-NT2RM1000462
- F-NT2RM1000542
Beta-galactosidase (GLB1)
1.3e-17:436:61
Hs.79222:M34423
- 10 F-NT2RM1000580
ESTs, Weakly similar to similar to M. musculus MER5 and other AHPC/TSA proteins [C.elegans]
6.2e-51:254:98
Hs.132096:AA314601
- 15 F-NT2RM1000789
Homo sapiens mRNA for hTCF-4
3.5e-96:299:92
Hs.154485:Y11306
- 20 F-NT2RM1000855
Hydroxysteroid (11-beta) dehydrogenase 2
0.021:178:67
Hs.1376:U26726
- 25 F-NT2RM1000858
- 30 F-NT2RM1000899
Homo sapiens BAC clone RG119C02 from 7p15
0.037:222:63
Hs.22900:AC004520
- 35 F-NT2RM2000241
ESTs
2.9e-31:166:97
Hs.156175:AI334328
- 40 F-NT2RM2000306
- F-NT2RM2000410
ESTs
3.2e-12:81:97
Hs.72116:AA151564
- 45 F-NT2RM2000423
Beta-galactosidase (GLB1)
0.074:163:63
Hs.79222:M34423
- 50 F-NT2RM2000497
ESTs, Weakly similar to CHL1 protein [H.sapiens]
3.7e-21:121:97
Hs.97515:AA435715
- 55 F-NT2RM2000514

F-NT2RM2000565

F-NT2RM2000582

EST

1.7e-42:218:98

Hs.160262:AI146610

F-NT2RM2000589

F-NT2RM2000622

Androgen receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease)

0.00018:409:62

Hs.99915:M23263

F-NT2RM2000632

Homo sapiens TBP-associated factor 172 (TAF-172) mRNA, complete cds

0.00017:331:59

Hs.14244:AF038362

F-NT2RM2000773

Human zinc finger protein (MAZ) mRNA

7.2e-47:274:91

Hs.7647:M94046

F-NT2RM2001126

Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds

5.1e-163:663:99

Hs.21301:AF093419

F-NT2RM2001558

Homo sapiens protein kinase A binding protein AKAP110 mRNA, complete cds

3.9e-166:770:98

Hs.98397:AF093408

F-NT2RM2001626

Human mRNA for KIAA0231 gene, partial cds

2.8e-40:562:67

Hs.7938:D86984

F-NT2RM2001643

ESTs

7.9e-112:548:97

Hs.12610:W56112

F-NT2RM2001738

FACTOR VIII INTRON 22 PROTEIN

0.32:452:59

Hs.83363:M34677

F-NT2RM2001767

Homo sapiens mRNA for B120, complete cds

5.0e-24:131:100

Hs.123090:AB001895

F-NT2RM2001792

Homo sapiens mRNA for serum lectin P35, complete cds

8.2e-14:244:67

Hs.54517:D63160

F-NT2RM2001818
EST
5 0.051:152:61
Hs.157619:AI357718

F-NT2RM2001902
Human p21-activated protein kinase (Pak1) gene, complete cds
10 4.4e-39:568:66
Hs.62402:U24152

F-NT2RM2001939
Human G protein-coupled receptor GPR-NGA gene, complete cds
15 4.2e-141:664:98
Hs.92458:U55312

F-NT2RM2001941
Dopamine receptor D4
20 1.3e-14:547:61
Hs.99922:L12398

F-NT2RM4000100
Human involucrin mRNA
25 1.1e-09:487:62
Hs.157091:M13903

F-NT2RM4000115

30 F-NT2RM4000198
ESTs
9.3e-101:496:98
Hs.128676:AA464413

35 F-NT2RM4000284
Human IgG Fc receptor hFcRn mRNA, complete cds
2.4e-38: 194:98
Hs.110804:U12255

40 F-NT2RM4000295
Homo sapiens SOX22 protein (SOX22) mRNA, complete cds
1.7e-06:479:60
Hs.43627:U35612

45 F-NT2RM4000326
Phosphorylase kinase, gamma 2 (testis)
0.95:204:63
Hs.87452:M31606

50 F-NT2RM4000417
H.sapiens Syt V gene (genomic and cDNA sequence)
0.97:143:67
Hs.23179:X96783

55 F-NT2RM4000444
Eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
0.45:194:64
Hs.90319:Z21507

- F-NT2RM4000587
Human proto-oncogene (FRAT1) gene, complete cds
3.8e-05:495:60
Hs.143005:U58975
- 5 F-NT2RM4000593
- F-NT2RM4000648
Homo sapiens glypican-4 (GPC4) mRNA, complete cds
1.0e-50:610:70
Hs.58367:AF030186
- 10 F-NT2RM4000761
EST
0.89:53:79
Hs.161967:AA494423
- 15 F-NT2RM4000965
H.sapiens mRNA for PHAPI2b protein
0.18:148:68
Hs.84264:U70439
- 20 F-NT2RM4000997
- 25 F-NT2RM4001321
ESTs
1.8e-94:467:97
Hs.12610:W56112
- 30 F-NT2RM4001325
Homo sapiens mRNA for chondroitin 6-sulfotransferase, complete cds
2.1e-13:384:64
Hs.158304:AB012192
- 35 F-NT2RM4001377
Homo sapiens mRNA for KIAA0638 protein, partial cds
3.1e-156:719:99
Hs.77864:AB014538
- 40 F-NT2RM4001735
- F-NT2RM4001768
ESTs
0.00012:123:68
Hs.128045:AA970231
- 45 F-NT2RM4001843
- F-NT2RM4002352
Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds
4.4e-157:761:97
Hs.143641:AB009462
- 50 F-NT2RP1000002
EST
0.00023:170:68
Hs.135504:AI091717
- 55

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- 5 F-NT2RP1000050
Histidine-rich calcium binding protein
0.0047:257:61
Hs.1480:M60052
- 10 F-NT2RP1000181
Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene
6.9e-99:510:94
Hs.132898:AC004770
- 15 F-NT2RP1000239
ESTs
1.7e-34:240:67
Hs.33020:N31946
- 20 F-NT2RP1000261
ESTs, Weakly similar to HYPOTHETICAL 25.2 KD PROTEIN IN ACB1-KSS1 INTERGENIC REGION [S.cerevisiae]
9.1e-92:484:94
Hs.7870:AI078137
- 25 F-NT2RP1000271
Homo sapiens DNA-binding protein mRNA, complete cds
1.4e-140:678:97
Hs.137582:AF038951
- 30 F-NT2RP1000300
Human endosome-associated protein (EEA1) mRNA, complete cds
1.0:205:61
Hs.2864:L40157
- 35 F-NT2RP1000325
Phosphate carrier, mitochondrial
7.7e-84:444:93
Hs.78713:X60036
- 40 F-NT2RP1000448
ESTs
9.5e-73:405:93
Hs.24054:N46499
- 45 F-NT2RP1000465
ESTs
8.5e-10:81:87
Hs.18619:AI202769
- 50 F-NT2RP1000468
Homo sapiens clone 24781 mRNA sequence
2.1e-20:133:92
Hs.108112:AF070640
- 55 F-NT2RP1000551
Homo sapiens putative interferon-related protein (SM15) mRNA, partial cds
2.4e-140:742:93
Hs.75402:U09585
- F-NT2RP1000579
SUCCINATE DEHYDROGENASE

- 1.1e-141:798:91
Hs.469:L21936
- 5 F-NT2RP1000613
Homo sapiens carbonic anhydrase precursor (CA 12) mRNA, complete cds
5.5e-11:468:58
Hs.5338:AF037335
- 10 F-NT2RP1000679
ESTs
0.79:127:65
Hs.146093:AA100242
- 15 F-NT2RP1000740
Homo sapiens Trio isoform mRNA, complete cds
0.24:160:66
Hs.150625:AF091395
- 20 F-NT2RP1000903
F-NT2RP1000981
- 25 F-NT2RP1001004
Human mRNA for Doc2 beta, complete cds
0.00072:520:57
Hs.54402:D70830
- 30 F-NT2RP1001020
ESTs, Weakly similar to SPORULATION-SPECIFIC PROTEIN 1 [*Saccharomyces cerevisiae*]
2.1e-73:392:94
Hs.4789:AI418298
- 35 F-NT2RP1001031
Miller-Dieker syndrome chromosome region
4.5e-07:383:61
Hs.77318:L13385
- 40 F-NT2RP1001563
Human eukaryotic translation initiation factor (eIF3) mRNA, complete cds
0.086:398:59
Hs.57783:U78525
- 45 F-NT2RP2000092
Zinc finger protein 136 (clone pHZ-20)
5.5e-56:652:70
Hs.69740:U09367
- 50 F-NT2RP2000178
Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence
0.14:231:62
Hs.159402:AC005609
- 55 F-NT2RP2000240
Homo sapiens KIAA0415 mRNA, complete cds
3.0e-61:554:76
Hs.7289:AB007875
- F-NT2RP2000394

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- ESTs
0.0063:210:63
Hs.134272:AI220363
- 5 F-NT2RP2000447
Human (clone SY11) golgin-95 mRNA, complete cds
3.8e-22:498:65
Hs.24049:L06147
- 10 F-NT2RP2000479
ESTs
1.3e-46:298:90
Hs.15641:W63676
- 15 F-NT2RP2000514
Homo sapiens roundabout 1 (robo1) mRNA, complete cds
1.2e-37:543:67
Hs.36702:AF040990
- 20 F-NT2RP2000533
ESTs, Highly similar to HYPOTHETICAL 16.3 KD PROTEIN IN DUR1,2-NGR1 INTERGENIC REGION [*Saccharomyces cerevisiae*]
5.4e-132:647:96
Hs.18120:AA913148
- 25 F-NT2RP2000610
Homo sapiens antigen NY-CO-16 mRNA, complete cds
0.00027:182:66
Hs.132206:AF039694
- 30 F-NT2RP2000616
ESTs
0.44:235:60
Hs.31714:AA514389
- 35 F-NT2RP2000649
Homo sapiens mRNA for Hs Ste24p, complete cds
6.2e-167:802:97
Hs.25846:AB016068
- 40 F-NT2RP2000663
Homo sapiens mRNA for KIAA0512 protein, complete cds
4.8e-15:305:64
Hs.48924:AB011084
- 45 F-NT2RP2000694
H.sapiens 5T4 gene for 5T4 Oncofetal antigen
1.0e-113:558:96
Hs.82128:AJ012159
- 50 F-NT2RP2000712
ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]
1.5e-83:442:93
Hs.154226:AA468767
- 55 F-NT2RP2000739
Human mRNA for KIAA0326 gene, partial cds
2.1e-25:574:62

- Hs.6833:AB002324
- F-NT2RP2000818
- 5 F-NT2RP2000903
H.sapiens 5T4 gene for 5T4 Oncofetal antigen
3.5e-112:539:97
Hs.82128:AJ012159
- 10 F-NT2RP2001200
Homo sapiens mRNA for KIAA0676 protein, partial cds
1.1e-111:540:96
Hs.115763:AB014576
- 15 F-NT2RP2001223
ESTs
5.9e-91:461:95
Hs.103733:AA436929
- 20 F-NT2RP2001276
Homo sapiens mRNA for KIAA0634 protein, partial cds
2.4e-11:382:62
Hs.30898:AB014534
- 25 F-NT2RP2001388
- F-NT2RP2001469
ESTs
7.3e-39:213:95
- 30 Hs.151001:AA564706
- F-NT2RP2001480
Homo sapiens thrombospondin 3 (THBS3) gene, complete cds
2.9e-141:686:96
- 35 Hs.82165:L38969
- F-NT2RP2001495
Human transporter protein (g17) mRNA, complete cds
6.0e-37:581:64
- 40 Hs.76460:U49082
- F-NT2RP2001514
- F-NT2RP2001529
Homo sapiens mRNA for ZIP-kinase, complete cds
1.5e-153:757:96
Hs.25619:AB007144
- 45
- F-NT2RP2001538
ESTs, Highly similar to co-repressor protein [M.musculus]
4.4e-63:329:94
Hs.22583:AA188168
- 50
- F-NT2RP2001562
Homo sapiens GLE1 (GLE1) mRNA, complete cds
7.5e-119:572:97
Hs.81449:AF058922
- 55

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- 5 F-NT2RP2001662
H.sapiens mRNA for TGIF protein
2.6e-29:448:67
Hs.90077:X89750
- 10 F-NT2RP2001755
ESTs, Highly similar to F-SPONDIN PRECURSOR [Rattus norvegicus]
1.0e-47:275:92
Hs.153657:H37929
- 15 F-NT2RP2001769
Human protein kinase C-L (PRKCL) mRNA, complete cds
1.9e-09:399:59
Hs.89616:M55284
- 20 F-NT2RP2001817
EST
0.97:133:63
Hs.145274:AI249468
- 25 F-NT2RP2001878
Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds
3.6e-05:491:60
Hs.159234:U89995
- 30 F-NT2RP2001903
Human mRNA for apolipoprotein E receptor 2, complete cds
0.0023:270:60
Hs.54481:D86407
- 35 F-NT2RP2001915
Homo sapiens Pig3 (PIG3) mRNA complete cds
3.2e-05:493:60
Hs.50649:AF010309
- 40 F-NT2RP2001921
- 45 F-NT2RP2001948
ESTs
0.55:213:61
Hs.147805:AI221717
- 50 F-NT2RP2001956
ESTs, Weakly similar to HYPOTHETICAL 25.2 KD PROTEIN IN ACB1-KSS1 INTERGENIC REGION [S.cerevisiae]
8.1e-45:510:70
Hs.13144:T67556
- 55 F-NT2RP2002015
ESTs
4.3e-20:127:92
Hs.12610:W56112
- F-NT2RP2002063
ESTs
1.0e-08:73:91
Hs.19814:T81721

F-NT2RP2002188

F-NT2RP2002232
EST
5 0.82:99:67
Hs.148596:AI202232

F-NT2RP2002304
Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds
10 0.031:107:71
Hs.82210:U47742

F-NT2RP2002409
Homo sapiens lymphocyte secreted C-type lectin precursor, mRNA, complete cds
15 0.00063:302:65
Hs.105927:AF020044

F-NT2RP2002510
ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galacto-
20 syltransferase)
4.4e-09:298:64
Hs.144023:U15197

F-NT2RP2002527
25 Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene
5.2e-65:327:96
Hs.132898:AC004770

F-NT2RP2002533
30 Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete
cds
2.1e-142:726:95
Hs.127436:AF040709

F-NT2RP2002564
35 Homo sapiens mRNA for repressor protein, partial cds
3.5e-55:594:74
Hs.58167:D30612

F-NT2RP2002674
40 Epoxide hydrolase 2, cytoplasmic
2.5e-07:332:62
Hs.113:L05779

F-NT2RP2002721

F-NT2RP2002824
ESTs, Weakly similar to ZK858.6 [C.elegans]
5.2e-28:190:90
50 Hs.120416:AA057428

F-NT2RP2002942
Homo sapiens mRNA for KIAA0806 protein, complete cds
2.0e-146:758:94
55 Hs.24279:AB018349

F-NT2RP2002974
ESTs

- 4.9e-51:475:77
Hs.137840:AI123378
- 5 F-NT2RP2002976
ESTs, Weakly similar to No definition line found [C.elegans]
7.8e-50:315:89
Hs.159604:AI380827
- 10 F-NT2RP2003042
Lecithin-cholesterol acyltransferase
2.4e-25:454:65
Hs.112125:M12625
- 15 F-NT2RP2003138
H.sapiens mRNA for TGIF protein
2.0e-05:121:75
Hs.90077:X89750
- 20 F-NT2RP2003179
Homo sapiens mRNA for KIAA0537 protein, complete cds
1.0e-43:587:70
Hs.12836:AB011109
- 25 F-NT2RP2003210
- F-NT2RP2003302
Zinc finger protein 136 (clone pHZ-20)
1.8e-64:691:69
Hs.69740:U09367
- 30 F-NT2RP2003369
Homo sapiens chromosome 7q22 sequence
5.1e-109:539:96
Hs.125742:AF053356
- 35 F-NT2RP2003383
Homo sapiens mRNA for KIAA0458 protein, complete cds
1.6e-159:801:95
Hs.7414:AB007927
- 40 F-NT2RP2003390
Homo sapiens SEC63 (SEC63) mRNA, complete cds
2.2e-116:554:98
Hs.31575:AF100141
- 45 F-NT2RP2003469
ESTs
0.26:127:69
Hs.62649:AA115328
- 50 F-NT2RP2003545
ESTs, Highly similar to SERINE/THREONINE-PROTEIN KINASE PAK [Rattus norvegicus]
4.2e-111:550:96
Hs.85768:W16504
- 55 F-NT2RP2003593
EST
8.7e-43:213:99

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- Hs.130657:AI005473
- F-NT2RP2003599
ESTs
5 7.8e-14:84:98
Hs.107171:H53973
- F-NT2RP2003655
- 10 F-NT2RP2003664
Homo sapiens mRNA for leptin receptor gene-related protein
5.4e-134:630:98
Hs.23581:Y12670
- 15 F-NT2RP2003931
Human mRNA for KIAA0365 gene, partial cds
4.3e-14:101:92
Hs.84123:AB002363
- 20 F-NT2RP2003940
Zinc finger protein 43 (HTF6)
4.6e-99:693:82
Hs.74107:X59244
- 25 F-NT2RP2003950
Cell division cycle 25A
0.00041:419:59
Hs.1634:M81933
- 30 F-NT2RP2004069
ESTs, Weakly similar to HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II [C.elegans]
1.3e-75:390:94
Hs.13322:AA151730
- 35 F-NT2RP2004108
Zinc finger protein 136 (clone pHZ-20)
4.9e-69:548:78
Hs.69740:U09367
- 40 F-NT2RP2004141
TRICHOHYALIN
4.8e-11:435:63
Hs.82276:L09190
- 45 F-NT2RP2004179
ESTs
0.0054:180:66
Hs.134917:AI092952
- 50 F-NT2RP2004205
Homo sapiens nuclear dual-specificity phosphatase (SBF1) mRNA, partial cds
0.27:474:56
Hs.112049:U93181
- 55 F-NT2RP2004447
Homo sapiens LDL receptor member LR3 mRNA, complete cds
0.016:456:57
Hs.6347:AF077820

- 5 F-NT2RP2004495
Human transporter protein (g17) mRNA, complete cds
1.2e-26:497:61
Hs.76460:U49082
- 10 F-NT2RP2004524
Human bone morphogenetic protein-3b
0.0016:259:64
Hs.2171:D49493
- 15 F-NT2RP2004556
ESTs
1.1e-34:181:97
Hs.27160:AA421991
- 20 F-NT2RP2004606
Tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)
5.7e-107:587:92
Hs.148726:X03124
- 25 F-NT2RP2004648
TUBULIN ALPHA-4 CHAIN
0.59:186:61
Hs.75318:X06956
- 30 F-NT2RP2004670
Human mRNA for KIAA0369 gene, complete cds
0.097:309:61
Hs.21355:AB002367
- 35 F-NT2RP2004794
ESTs
1.3e-60:310:96
Hs.84926:N50073
- 40 F-NT2RP2004837
- 45 F-NT2RP2004847
Zinc finger protein 42 (myeloid-specific retinoic acid-responsive)
1.4e-05:396:60
Hs.78247:M58297
- 50 F-NT2RP2005027
GLUCOSE TRANSPORTER TYPE 3, BRAIN
7.2e-147:713:96
Hs.7594:M20681
- 55 F-NT2RP2005069
Human mRNA for KIAA0355 gene, complete cds
0.14:303:61
Hs.153014:AB002353
- F-NT2RP2005163
ESTs, Weakly similar to No definition line found [C.elegans]
1.4e-23:334:70
Hs.159604:AI380827
- F-NT2RP2005181

- Ecotropic retroviral receptor
8.3e-45:501:70
Hs.2928:X57303
- 5 F-NT2RP2005247
Oxysterol binding protein
4.2e-08:356:62
Hs.143065:M86917
- 10 F-NT2RP2005378
ESTs
1.7e-100:485:97
Hs.151572:AA588083
- 15 F-NT2RP2005391
EST
1.0:264:62
Hs.148259:AA905706
- 20 F-NT2RP2005425
Homo sapiens mRNA for KIAA0803 protein, partial cds
3.3e-118:566:97
Hs.58103:AB018346
- 25 F-NT2RP2005463
- F-NT2RP2005514
ESTs
3.6e-18:193:77
- 30 Hs.153344:R26293
- F-NT2RP2005535
Homo sapiens DNA-binding protein mRNA, complete cds
7.5e-127:726:90
- 35 Hs.137582:AF038951
- F-NT2RP2005541
Glucosamine (N-acetyl)-6-sulfatase (Sanfilippo disease IIID)
1.2e-06:225:64
- 40 Hs.2703:Z12173
- F-NT2RP2005597
- F-NT2RP2005632
ESTs
5.6e-67:344:96
- 45 Hs.112011:AA987961
- F-NT2RP2005666
ESTs
5.8e-71:453:87
- 50 Hs.122698:AI042484
- F-NT2RP2005774
Zinc finger protein 136 (clone pHZ-20)
1.3e-45:451:74
- 55 Hs.69740:U09367

F-NT2RP2005878
 ESTs, Highly similar to ESTRADIOL 17 BETA-DEHYDROGENASE 3 [Homo sapiens]
 5.9e-10:67:100
 Hs.104523:AA584520
 5

F-NT2RP2005883
 F-NT2RP2005887

10 F-NT2RP2005941
 Human novel homeobox mRNA for a DNA binding protein
 6.2e-11:464:61
 Hs.37035:U07664

15 F-NT2RP2005994
 F-NT2RP2006004
 Homo sapiens KIAA0405 mRNA, complete cds
 1.2e-13:273:63
 20 Hs.48998:AB007865

F-NT2RP2006042
 Human mRNA for KIAA0144 gene, complete cds
 5.6e-12:220:69
 25 Hs.8127:D63478

F-NT2RP2006092
 Human FE65-like protein (hFE65L) mRNA, partial cds
 2.6e-23:353:65
 30 Hs.24957:U62325

F-NT2RP2006099
 EST
 2.5e-28:180:90
 35 Hs.160878:AI361890

F-NT2RP2006134
 Neogenin (chicken) homolog 1
 0.035:219:60
 40 Hs.90408:U61262

F-NT2RP2006269
 Homo sapiens mRNA for matrilin-3
 1.0:147:65
 45 Hs.119534:AJ224741

F-NT2RP2006512
 ESTs
 1.6e-09:70:95
 50 Hs.118981:AA282396

F-NT2RP3000011
 F-NT2RP3000022
 55 EST
 0.016:293:60
 Hs.127706:AA961478

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5 F-NT2RP3000059
Human SH3 domain-containing proline-rich kinase (sprk) mRNA, complete cds
0.0041:608:59
Hs.89449:L32976

10 F-NT2RP3000063
Excision repair protein ERCC6
1.0:264:59
Hs.99924:L04791

15 F-NT2RP3000125
Human mRNA for KIAA0314 gene, partial cds
6.9e-08:379:59
Hs.155045:AB002312

20 F-NT2RP3000148
Human Chromosome 16 BAC clone CIT987SK-A-635H12
4.5e-40:349:73
Hs.108604:AC002310

25 F-NT2RP3000169
Homo sapiens MRS1 mRNA, complete cds
1.1e-107:501:99
Hs.30985:AF093239

30 F-NT2RP3000171
Homo sapiens methionine synthase reductase (MTRR) mRNA, complete cds
1.0:279:64
Hs.153792:AF025794

35 F-NT2RP3000172
Homo sapiens mRNA for ZIP-kinase, complete cds
7.4e-09:463:59
Hs.25619:AB007144

40 F-NT2RP3000201
Homo sapiens mRNA for KIAA0687 protein, partial cds
3.0e-171:792:98
Hs.3628:AB014587

45 F-NT2RP3000232
ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]
8.6e-24:304:70
Hs.112094:AA447558

50 F-NT2RP3000304
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds
1.1e-172:797:98
Hs.23672:AF074264

55 F-NT2RP3000378
Homo sapiens mRNA for KIAA0700 protein, partial cds
4.3e-45:585:66
Hs.13999:AB014600

F-NT2RP3000427
Protein kinase, cAMP-dependent, catalytic, beta
1.2e-15:97:98

- Hs.87773:M34181
- F-NT2RP3000436
Human protein disulfide isomerase-related protein P5 mRNA, partial cds
5 4.1e-06:353:59
Hs.85200:D49489
- F-NT2RP3000444
Homo sapiens mRNA for KIAA0445 protein, complete cds
10 1.2e-08:542:60
Hs.154139:AB007914
- F-NT2RP3000460
ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]
15 1.3e-17:181:75
Hs.131840:AI016073
- F-NT2RP3000481
Homo sapiens RanBP7/importin 7 mRNA, complete cds
20 5.4e-164:770:98
Hs.5151:AF098799
- F-NT2RP3000616
Homo sapiens KIAA0405 mRNA, complete cds
25 1.5e-32:579:62
Hs.48998:AB007865
- F-NT2RP3000645
Human KH type splicing regulatory protein KSRP mRNA, complete cds
30 4.6e-06:245:64
Hs.91142:U94832
- F-NT2RP3000652
Homo sapiens DNA from chromosome 19, BAC 33152
35 2.6e-135:853:84
Hs.55452:AC003973
- F-NT2RP3000676
Homo sapiens mRNA for KIAA0446 protein, complete cds
40 8.8e-88:420:98
Hs.158286:AB007915
- F-NT2RP3000677
ESTs
45 3.9e-09:67:97
Hs.98819:AA778727
- F-NT2RP3000721
ESTs, Weakly similar to No definition line found [C.elegans]
50 1.2e-57:395:86
Hs.159604:AI380827
- F-NT2RP3000789
Homo sapiens putative RNA binding protein KOC (koc) mRNA, complete cds
55 4.8e-75:833:69
Hs.79440:U97188
- F-NT2RP3000818

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- Homo sapiens chromosome 19, fosmid 39554
5.9e-08:313:63
Hs.129906:AC004410
- 5 F-NT2RP3000820
ESTs, Moderately similar to WSB-1 [M.musculus]
8.8e-127:613:97
Hs.24630:AI365246
- 10 F-NT2RP3000838
Homo sapiens mRNA for KIAA0638 protein, partial cds
8.3e-79:682:79
Hs.77864:AB014538
- 15 F-NT2RP3000871
Homo sapiens retinoblastoma-interacting protein (RBBP8) mRNA, complete cds
1.9e-08:350:60
Hs.29287:U72066
- 20 F-NT2RP3000907
Human Ini1 mRNA, complete cds
0.91:345:59
Hs.155626:U04847
- 25 F-NT2RP3000921
Homo sapiens mRNA for KIAA0806 protein, complete cds
2.0e-65:798:68
Hs.24279:AB018349
- 30 F-NT2RP3001012
Homo sapiens mRNA for KIAA0667 protein, partial cds
1.3e-21:383:64
Hs.154740:AB014567
- 35 F-NT2RP3001044

F-NT2RP3001061
KERATIN, TYPE II CYTOSKELETAL 7
3.4e-05:256:62
40 Hs.23881:M99063

F-NT2RP3001159
Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene
1.8e-81:527:70
45 Hs.132874:AC004770

F-NT2RP3001170
Homo sapiens mRNA for KIAA0784 protein, partial cds
7.3e-183:859:98
50 Hs.3657:AB018327

F-NT2RP3001 195
ESTs
3.5e-08:282:62
55 Hs.135168:AI394026

F-NT2RP3001240
ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]

- 2.8e-64:344:95
Hs.14038:R06800
- 5 F-NT2RP3001271
Centromere protein B (80kD)
7.6e-08:288:64
Hs.85004:X05299
- 10 F-NT2RP3001322
ESTs, Weakly similar to W09D10.2 [C.elegans]
1.2e-86:422:98
Hs.26107:R60661
- 15 F-NT2RP3001388
F-NT2RP3001542
F-NT2RP3001560
Protein phosphatase 2C alpha [human, teratocarcinoma, mRNA, 2346 nt]
20 0.016:190:63
Hs.57764:S87759
- 25 F-NT2RP3001592
Cyclin-dependent kinase inhibitor 1C (p57, Kip2)
2.3e-13:188:71
Hs.106070:U22398
- 30 F-NT2RP3001650
Homo sapiens KIAA0415 mRNA, complete cds
1.6e-17:394:66
Hs.7289:AB007875
- 35 F-NT2RP3001685
F-NT2RP3001738
Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene
1.9e-54:776:65
Hs.132898:AC004770
- 40 F-NT2RP3001754
Homo sapiens mRNA for B120, complete cds
2.4e-18:106:100
Hs.123090:AB001895
- 45 F-NT2RP3001858
Homo sapiens mRNA for KIAA0584 protein, partial cds
1.9e-40:770:63
Hs.106794:AB011156
- 50 F-NT2RP3001976
Zinc finger protein 140 (clone pHZ-39)
7.3e-33:493:68
Hs.154205:U09368
- 55 F-NT2RP3002015
Homo sapiens OPA-containing protein mRNA, complete cds
0.018:329:62
Hs.85313:AF071309

F-NT2RP3002160
Homo sapiens protein phosphatase with EF-hands-2 long form (PPEF-2) mRNA, complete cds
0.53:182:64
Hs.113259:AF023456

5

F-NT2RP3002281
Homo sapiens mRNA for KIAA0765 protein, partial cds
5.2e-151:713:98
Hs.62318:AB018308

10

F-NT2RP3002286
ESTs
0.034:48:95
Hs.124692:AA777421

15

F-NT2RP3002311
Beta-galactosidase (GEB1)
2.3e-28:633:61
Hs.79222:M34423

20

F-NT2RP3002324
ESTs
2.5e-28:296:75
Hs.22822:H06408

25

F-NT2RP3002342
Human transporter protein (g17) mRNA, complete cds
3.2e-37:565:65
Hs.76460:U49082

30

F-NT2RP3002353
Homo sapiens mRNA for KIAA0790 protein, partial cds
0.0055:271:60
Hs.12002:AB018333

35

F-NT2RP3002409
Homo sapiens mRNA for KIAA0719 protein, complete cds
6.4e-191:897:98
Hs.21198:AB018262

40

F-NT2RP3002411
Hydroxysteroid (17-beta) dehydrogenase 3
2.9e-28:604:62
Hs.477:U05659

45

F-NT2RP3002448
Human mRNA for KIAA0233 gene, complete cds
1.6e-08:721:57
Hs.79077:D87071

50

F-NT2RP3002571
Homo sapiens mRNA for KIAA0603 protein, complete cds
9.7e-67:707:71
Hs.16909:AB011175

55

F-NT2RP3002664
Homo sapiens Trio isoform mRNA, complete cds
0.26:160:66

Hs.150625:AF091395

F-NT2RP3002721

Homo sapiens citrate synthase mRNA, complete cds

2.4e-180:873:96

Hs.132991:AF047042

F-NT2RP3002737

Homo sapiens mRNA for voltage gated potassium channel

7.1e-43:409:75

Hs.4975:Y15065

F-NT2RP3002738

Human BMK1 alpha kinase mRNA, complete cds

0.0070:722:57

Hs.3080:U29725

F-NT2RP3002790

Cyclin-dependent kinase inhibitor 1C (p57, Kip2)

7.2e-17:626:62

Hs.106070:U22398

F-NT2RP3002836

Homo sapiens mRNA for KIAA0463 protein, partial cds

2.2e-153:717:99

Hs.77738:AB007932

F-NT2RP3002887

Human plectin (PLEC1) mRNA, complete cds

2.5e-06:605:59

Hs.79706:U53204

F-NT2RP3002900

H.sapiens mRNA for transmembrane protein rnp24

3.1e-09:346:64

Hs.75914:X92098

F-NT2RP3002958

ESTs

8.3e-117:765:86

Hs.107119:AI198794

F-NT2RP3002983

ESTs

1.4e-07:270:67

Hs.160271:AI149075

F-NT2RP3003000

Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds

2.5e-89:555:88

Hs.122359:AF051946

F-NT2RP3003076

Homo sapiens mRNA for APC 2 protein, complete cds

0.00016:522:60

Hs.20912:AB012162

F-NT2RP3003354

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Homo sapiens secretory carrier membrane protein (SCAMP2) mRNA, complete cds
4.0e-36:625:64
Hs.10761:AF005038

- 5 F-NT2RP3003448
Arginine vasopressin receptor 1B
0.77:149:69
Hs.1372:L37112
- 10 F-NT2RP3003469
ESTs
1.4e-42:239:93
Hs.12610:W56112
- 15 F-NT2RP3003473
ESTs, Highly similar to transcription factor ARF6 chain B [M.musculus]
8.7e-46:281:89
Hs.136172:W28257
- 20 F-NT2RP3003527
Homo sapiens mRNA for protein kinase Dyrk1B
4.6e-162:769:98
Hs.130988:Y17999
- 25 F-NT2RP3003532
OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR
1.5e-146:682:98
Hs.79015:M17229
- 30 F-NT2RP3003535
EST
6.7e-10:330:60
Hs.133239:AI052508
- 35 F-NT2RP3003559
Breakpoint cluster region protein BCR
1.0:143:66
Hs.2557:Y00661
- 40 F-NT2RP3003614
ESTs
3.7e-50:327:88
Hs.148873:T33582
- 45 F-NT2RP3003729
ESTs, Weakly similar to unknown [S.cerevisiae]
1.9e-96:449:99
Hs.100843:W28953
- 50 F-NT2RP3003849
ESTs, Weakly similar to raphilin [M.musculus]
1.7e-32:197:92
Hs.118457:AA019161
- 55 F-NT2RP3003874
Homo sapiens incomplete cDNA for a myosin class I, myh-1c
8.5e-84:494:90
Hs.109805:AJ001381

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5 F-NT2RP3003939
Peroxisomal biogenesis factor 6
1.5e-05:236:62
Hs.30729:D83703

10 F-NT2RP3003963

F-NT2RP3004000
Homo sapiens mRNA for APC 2 protein, complete cds
4.8e-06:669:59
Hs.20912:AB012162

15 F-NT2RP3004025
ESTs
0.0015:68:86
Hs.154835:AI289188

20 F-NT2RP3004067
ESTs, Weakly similar to HYPOTHETICAL 51.2 KD PROTEIN IN LAG1-RPL14B INTERGENIC REGION [S.cere-
visiae]
2.1e-76:416:94
Hs.9252:R53360

25 F-NT2RP3004075
ESTs
1.1e-54:298:94
Hs.124051:T15786

30 F-NT2RP3004083

F-NT2RP3004090
Homo sapiens Achaete-Scute homologue 2 (ASCL2) gene, complete cds
2.4e-06:486:62
Hs.135639:U77629

35 F-NT2RP3004119
Human mRNA for KIAA0215 gene, complete cds
4.1e-74:640:75
Hs.82292:D86969

40 F-NT2RP3004130

F-NT2RP3004133
ESTs, Weakly similar to similar to M. musculus MER5 and other AHPC/TSA proteins [C.elegans]
4.6e-52:259:98
Hs.132096:AA314601

45 F-NT2RP3004202
ALPHA-2C-1 ADRENERGIC RECEPTOR
1.0:229:62
Hs.123022:J03853

50 F-NT2RP3004294
Homo sapiens mRNA for KIAA0741 protein, complete cds
2.4e-05:404:59
Hs.3615:AB018284

55 F-NT2RP3004309

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Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC269730) containing the hFEN1 gene
3.4e-71:756:71
Hs.132874:AC004770

- 5 F-NT2RP3004321
Homo sapiens (clone MG2-5-12) mucin (MG2) mRNA, complete polyA site
0.015:263:60
Hs.103944:L13283
- 10 F-NT2RP3004345
Cyclin-dependent kinase inhibitor 1C (p57, Kip2)
2.3e-13:188:71
Hs.106070:U22398
- 15 F-NT2RP3004355
EST
0.25:130:59
Hs.149436:AI274484
- 20 F-NT2RP3004374
ESTs
1.4e-95:480:96
Hs.12610:W56112
- 25 F-NT2RP3004406
Human breast cancer, estrogen regulated LIV-1 protein (LIV-1) mRNA, partial cds
3.4e-45:505:70
Hs.79136:U41060
- 30 F-NT2RP3004481
Homo sapiens mRNA for KIAA0476 protein, complete cds
0.00065:594:58
Hs.6684:AB007945
- 35 F-NT2RP3004552
Biglycan
0.92:347:57
Hs.821:J04599
- 40 F-NT2RP3004557
Human Ki nuclear autoantigen mRNA, complete cds
2.6e-121:626:94
Hs.152978:U11292
- 45 F-NT2RP3004625
Homo sapiens I-1 receptor candidate protein mRNA, complete cds
3.1e-152:710:98
Hs.26285:AF082516
- 50 F-NT2RP3004640
ESTs, Moderately similar to unknown [H.sapiens]
0.76:195:64
Hs.6487:T65302
- 55 F-NT2RP3004647
Homo sapiens mRNA for KIAA0446 protein, complete cds
6.6e-111:524:98
Hs.158286:AB007915

- 5 F-NT2RP4000108
NEUROFILAMENT TRIPLET L PROTEIN
5.3e-159:862:93
Hs.159540:X05608
- 10 F-NT2RP4000634
Human MEK kinase 3 mRNA, complete cds
2.3e-54:370:71
Hs.86201:U78876
- 15 F-NT2RP4000962
ESTs, Weakly similar to SPORULATION-SPECIFIC PROTEIN 1 [Saccharomyces cerevisiae]
2.3e-95:479:96
Hs.4789:AI418298
- 20 F-NT2RP4001001
EST
0.98:93:64
Hs.147598:AI217868
- 25 F-NT2RP4001009
Homo sapiens mRNA for Hs Ste24p, complete cds
3.1e-176:828:98
Hs.25846:AB016068
- 30 F-NT2RP4001467
5' nucleotidase (CD73)
1.1e-160:742:98
Hs.153952:X55740
- 35 F-NT2RP4001877
ESTs, Weakly similar to siah binding protein 1 [H.sapiens]
3.3e-103:495:98
Hs.65648:AA600816
- 40 F-NT2RP4001879
EST
0.78:171:61
Hs.112790:AA609949
- 45 F-NT2RP4002187
Hydroxysteroid (17-beta) dehydrogenase 3
9.9e-27:534:63
Hs.477:U05659
- 50 F-NT2RP4002451
ESTs
1.5e-11:106:86
Hs.163724:AA017689
- 55 F-NT2RP4002715
EST
4.2e-07:64:93
Hs.160901:AI366910
- F-NT2RP4002750
Ecotropic retroviral receptor
6.6e-51:581:68

Hs.2928:X57303

F-OVARC1000003

Solute carrier family 17 (sodium phosphate), member 2

6.9e-65:587:73

Hs.936:L13258

F-OVARC1000090

ESTs

4.8e-07:214:65

Hs.87456:AA434484

F-OVARC1000105

Human novel homeobox mRNA for a DNA binding protein

0.00095:204:64

Hs.37035:U07664

F-OVARC1000137

Human SNARE protein Ykt6 (YKT6) mRNA, complete cds

4.0e-35:184:98

Hs.31531:U95735

F-OVARC1000208

Human calcium-dependent group X phospholipase A2 mRNA, complete cds

1.5e-61:365:90

Hs.136004:U95301

F-OVARC1000255

Spleen tyrosine kinase

2.2e-88:615:84

Hs.74101:L28824

F-OVARC1000275

ESTs, Weakly similar to Rap2 interacting protein 8 [M.musculus]

4.7e-85:424:97

Hs.55165:AA573499

F-OVARC1000298

Homo sapiens GABA-B receptor mRNA, complete cds

0.00021:285:61

Hs.12307:AF056085

F-OVARC1000307

ESTs

0.00016:226:63

Hs.162935:AI393970

F-OVARC1000313

Homo sapiens mRNA for KIAA0573 protein, partial cds

5.5e-121:585:97

Hs.154023:AB011145

F-OVARC1000331

Glucose-6-phosphate dehydrogenase

5.3e-18:213:71

Hs.1435:M24470

F-OVARC1000410

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Homo sapiens mRNA for angiopoietin-like factor
 1.5e-27:538:62
 Hs.146559:Y16132

5 F-OVARC1000439

F-OVARC1000467
 ESTs
 2.5e-26:173:90

10 Hs.105040:AA292817

F-OVARC1000529
 Homo sapiens mRNA for C8FW phosphoprotein
 1.1e-12:391:59

15 Hs.143513:AJ000480

F-OVARC1000553
 Homo sapiens chromosome 19, cosmid R26894
 9.0e-111:425:99

20 Hs.157732:AC005594

F-OVARC1000775
 Human chromosome 3p21.1 gene sequence
 2.2e-70:380:95

25 Hs.82837:L13435

F-OVARC1000811
 HEPATOCYTE GROWTH FACTOR ACTIVATOR PRECURSOR
 1.2e-06:446:61

30 Hs.104:D14012

F-OVARC1000853
 ESTs
 7.9e-09:268:63

35 Hs.92700:W37903

F-OVARC1000873
 Homo sapiens mRNA for MIFR-1, complete cds
 0.038:343:60

40 Hs.58269:AB010962

F-OVARC1000916
 H.sapiens PISSLRE mRNA
 1.3e-56:435:82

45 Hs.77313:X78342

F-OVARC1000956
 Human TBP-associated factor (hTAFII130) mRNA, partial cds
 7.7e-05:511:59

50 Hs.24644:U75308

F-OVARC1000995
 ESTs
 2.4e-39:205:98

55 Hs.163662:AA514348

F-OVARC1001030
 EST

1.1e-44:232:96
Hs.135504:AI091717

5 F-OVARC1001049
ESTs
6.1e-78:373:98
Hs.135022:AI417283

10 F-OVARC1001086
Homo sapiens cyclin T2a mRNA, complete cds
6.0e-166:761:99
Hs.155478:AF048731

15 F-OVARC1001132
ESTs, Weakly similar to GC-RICH SEQUENCE DNA-BINDING FACTOR [Homo sapiens]
7.9e-121:610:96
Hs.26461:AI341685

20 F-OVARC1001163
ESTs
5.9e-39:215:94
Hs.126067:AI344351

25 F-OVARC1001222
ESTs
2.7e-93:467:95
Hs.10267:W27845

30 F-OVARC1001260
Pregnancy-zone protein
1.0:251:58
Hs.74094:X54380

35 F-OVARC1001336
Solute carrier family 17 (sodium phosphate), member 2
1.2e-31:304:74
Hs.936:L13258

40 F-OVARC1001338
Homo sapiens cam kinase I mRNA, complete cds
3.7e-17:570:60
Hs.118414:L41816

45 F-OVARC1001569
Human novel homeobox mRNA for a DNA binding protein
0.038:178:63
Hs.37035:U07664

50 F-OVARC1001570
ESTs
4.5e-10:75:93
Hs.120928:AA703165

55 F-OVARC1001596
Matrix metalloproteinase 2 (gelatinase A, 72kD gelatinase, 72kD type IV collagenase)
0.0092:287:63
Hs.111301:M55593

- 5 F-OVARC1001607
Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds
5.5e-41:323:80
Hs.154844:U15128
- F-OVARC 1001725
- 10 F-OVARC1001727
EST
3.2e-05:237:61
Hs.119508:AA485732
- 15 F-OVARC1001807
Hormone receptor (growth factor-inducible nuclear protein N10)
3.4e-91:564:88
Hs.1119:D49728
- 20 F-OVARC1001833
ESTs
1.2e-94:444:97
Hs.155256:AA707750
- 25 F-OVARC1001952
Myristoylated alanine-rich C-kinase substrate
2.9e-10:364:64
Hs.75607:D10522
- 30 F-OVARC1001991
Human mRNA for KIAA0176 gene, partial cds
0.0019:224:62
Hs.4935:D79998
- 35 F-OVARC1002058
Human mRNA for KIAA0149 gene, complete cds
5.0e-48:674:67
Hs.57735:D86864
- 40 F-OVARC1002178
Homo sapiens zinc-finger protein of the cerebellum 3 (ZIC3) mRNA, complete cds
0.010:310:61
Hs.111227:AF028706
- F-PLACE1000033
- 45 F-PLACE1000231
Guanine nucleotide binding protein (G protein), alpha 11 (Gq class)
0.00021:235:63
Hs.1686:M69013
- 50 F-PLACE1000258
KRAB zinc finger protein {alternative products}
1.2e-14:241:70
Hs.22556:U37251
- 55 F-PLACE1000442
Zinc finger protein 136 (clone pHZ-20)
7.3e-89:774:76
Hs.69740:U09367

- 5
F-PLACE1000560
ESTs
1.5e-36:200:96
Hs.86541:AA214554
- 10
F-PLACE1000740
Homo sapiens secreted apoptosis related protein 3 (SARP3) mRNA, complete cds
6.5e-05:283:62
Hs.113285:AF017988
- 15
F-PLACE1000907
ESTs, Moderately similar to zinc finger protein [H.sapiens]
8.1e-38:237:89
Hs.139115:AA325104
- 20
F-PLACE1000912
ESTs
4.6e-61:331:95
Hs.17558:AA155762
- 25
F-PLACE1000914
Homo sapiens PB39 mRNA, complete cds
3.1e-45:500:69
Hs.18910:AF045584
- 30
F-PLACE1000927
ESTs, Weakly similar to N-methyl-D-aspartate receptor-associated protein [D.melanogaster]
1.4e-123:655:94
Hs.8661:AI189791
- 35
F-PLACE1000986
ESTs
1.2e-105:494:99
Hs.19207:AA039595
- 40
F-PLACE1001016
Calcium channel, voltage-dependent, L type, alpha 1S subunit
0.011:432:59
Hs.1294:L33798
- 45
F-PLACE1001100
Human clone 23839 mRNA sequence
0.38:342:60
Hs.78362:U79249
- 50
F-PLACE1001114
Human mRNA for KIAA0303 gene, partial cds
0.085:339:59
Hs.54985:AB002301
- 55
F-PLACE1041123
ESTs
5.0e-14:505:61
Hs.99272:AI147740
- F-PLACE1001183
ESTs, Weakly similar to gene pp21 protein [H.sapiens]
0.66:361:58

Hs.15984:A,1085974

F-PLACE1001229

ESTs, Weakly similar to D9481.15 gene product [S.cerevisiae]

9.3e-110:561:96

Hs.125155:W52093

F-PLACE1001231

ESTs, Weakly similar to sodium iodide symporter [H.sapiens]

1.0e-17:120:91

Hs.5167:AA053914

F-PLACE1001340

Homo sapiens mRNA for KIAA0719 protein, complete cds

4.1e-132:636:97

Hs.21198:AB018262

F-PLACE1001401

ESTs, Weakly similar to IgE receptor beta subunit [H.sapiens]

3.1e-100:516:95

Hs.43900:AA418443

F-PLACE 1001407

H.sapiens mRNA for B-HLH DNA binding protein

0.00015:244:66

Hs.66744:X99268

F-PLACE1001464

5' nucleotidase (CD73)

1.6e-152:742:96

Hs.153952:X55740

F-PLACE1001500

Bloom syndrome

5.7e-05:450:58

Hs.36820:U39817

F-PLACE1001516

Homo sapiens Rigui (RIGUI) mRNA, complete cds

2.3e-07:663:58

Hs.8114:AF022991

F-PLACE1001536

ESTs

4.6e-60:318:97

Hs.13026:H04491

F-PLACE1001564

H.sapiens mRNA for HE6 Tm7 receptor

8.8e-41:499:70

Hs.155681:X81892

F-PLACE1001655

Homo sapiens Shab-related delayed-rectifier K⁺ channel alpha subunit (KCNS3) mRNA, complete cds

4.3e-125:585:98

Hs.47584:AF043472

F-PLACE1001788

Homo sapiens mRNA for HYA22, complete cds
3.2e-22:234:75
Hs.147189:D88153

5 F-PLACE1001795

F-PLACE1001836
ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]
1.1e-18:162:80
10 Hs.157223:AA309318

F-PLACE1001918
Human p76 mRNA, complete cds
1.3e-22:693:60
15 Hs.28757:U81006

F-PLACE1001949
ESTs
0.97:243:63
20 Hs.151143:AA576926

F-PLACE1002080
Homo sapiens mRNA for KIAA0600 protein, partial cds
2.4e-130:622:98
25 Hs.9028:AF039691

F-PLACE1002095

F-PLACE1002153
Homo sapiens TACC2 protein (TACC2) mRNA, partial cds
2.7e-162:764:98
30 Hs.90415:AF095791

F-PLACE1002329
ESTs
1.5e-107:556:95
35 Hs.28907:AI343292

F-PLACE1002355
Homo sapiens protease-activated receptor 4 mRNA, complete cds
9.0e-19:190:77
40 Hs.137574:AF055917

F-PLACE1002374
Cathepsin L
2.0e-163:716:94
45 Hs.78056:X12451

F-PLACE1002518
Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds
7.0e-19:396:64
50 Hs.28285:AF064801

F-PLACE1002547
Homo sapiens mRNA for KIAA0719 protein, complete cds
8.3e-173:819:98
55 Hs.21198:AB018262

5 F-PLACE1002726
Human mRNA for KIAA0362 gene, partial cds
1.0:310:59
Hs.25515:AB002360

10 F-PLACE1002905
ESTs
2.4e-74:415:92
Hs.110298:AA621807

15 F-PLACE1002911
ESTs, Weakly similar to Y53C12A.3 [C.elegans]
0.030:279:58
Hs.107747:AI357868

20 F-PLACE1002967
ESTs
3.3e-120:574:98
Hs.11090:W37646

25 F-PLACE1003135
Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds
1.5e-50:450:75
Hs.72292:AF024636

30 F-PLACE1003163
Homo sapiens DBI-related protein mRNA, complete cds
1.5e-153:722:98
Hs.15250:AF069301

35 F-PLACE1003407
Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds
2.0e-142:682:97
Hs.30213:AF068227

40 F-PLACE1003428
Biotinidase
8.2e-06:265:62
Hs.78885:AF018631

45 F-PLACE1003438
ESTs
0.018:470:60
Hs.119482:AI361002

50 F-PLACE1003460
ESTs
0.019:211:60
Hs.92700:W37903

55 F-PLACE1003529
130 KD LEUCINE-RICH PROTEIN
0.53:208:63
Hs.87157:M92439

F-PLACE1003573
F-PLACE1003598

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Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
0.00064:302:64
Hs.96253:U79666

5 F-PLACE1003644
ESTs
1.3e-06:265:63
Hs.163564:R43678

10 F-PLACE1003737

F-PLACE1003772
Human p300/CBP-associated factor (P/CAF) mRNA, complete cds
7.0e-09:448:61
15 Hs.155302:U57317

F-PLACE1003839
Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69G12
7.7e-109:521:97
20 Hs.154050:AC004131

F-PLACE1003845
ESTs, Moderately similar to similar to thymidine diphosphoglucose 4,6-dehydratase [C.elegans]
1.2e-92:432:100
25 Hs.153778:AI246000

F-PLACE1003852
Homo sapiens mRNA for KIAA0758 protein, partial cds
2.4e-172:814:98
30 Hs.22039:AB018301

F-PLACE1004028

F-PLACE1004078
35 GELSOLIN PRECURSOR, PLASMA
3.1e-49:616:67
Hs.80562:X04412

F-PLACE1004166
40 ESTs
7.6e-79:415:94
Hs.163741:AA551077

F-PLACE1004168

45 F-PLACE1004199
EST
6.8e-15:147:80
Hs.128205:AA972308

50 F-PLACE1004279
Homo sapiens putative renal organic anion transporter 1 (hROAT1) mRNA, complete cds
3.9e-20:456:62
Hs.23965:AF057039

55 F-PLACE1004282

F-PLACE1004305

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- Homo sapiens mRNA for KIAA0740 protein, complete cds
8.7e-123:612:96
Hs.15099:AB018283
- 5 F-PLACE1004441
Human G protein-coupled receptor (GPR1) gene, complete cds
8.6e-99:501:96
Hs.159248:U13666
- 10 F-PLACE1004450
AMINOPEPTIDASE N
1.1e-09:587:57
Hs.1239:M22324
- 15 F-PLACE1004482

F-PLACE1004492
ESTs
2.1e-25:134:100
20 Hs.154475:AI199037

F-PLACE1004519
ESTs
1.0e-110:518:99
25 Hs.128505:AA306435

F-PLACE1004520
Pregnancy-specific beta 1-glycoprotein 7
1.3e-110:606:92
30 Hs.119662:M34715

F-PLACE1004630
Homo sapiens mRNA for osteoblast specific cysteine-rich protein, complete cds
2.0e-139:749:92
35 Hs.82582:AB008375

F-PLACE1004637

F-PLACE1004648
40

F-PLACE1004816
Homo sapiens mRNA for Hakata antigen, complete cds
1.2e-99:590:90
Hs.9225:D88587
45

F-PLACE1004887
Homo sapiens Achaete-Scute homologue 2 (ASCL2) gene, complete cds
5.1e-06:486:62
Hs.135639:U77629
50

F-PLACE1005003
Human SNC19 mRNA sequence
1.5e-21:472:63
Hs.56937:U20428
55

F-PLACE1005005
Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds
4.7e-42:245:93

- Hs.151614:AF032456
- F-PLACE1005031
ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [Bos taurus]
5 2.9e-43:538:70
Hs.118991:AA675919
- F-PLACE1005239
ESTs
10 2.4e-42:209:100
Hs.154475:AI199037
- F-PLACE1005250
- 15 F-PLACE1005383
Homo sapiens UP50 mRNA, complete cds
8.5e-128:633:96
Hs.11494:AF093118
- 20 F-PLACE1005410
ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]
1.3e-17:181:75
Hs.131840:AI016073
- 25 F-PLACE1005426
Pregnancy-specific beta-1 glycoprotein 4
2.3e-109:596:93
Hs.108936:X17097
- 30 F-PLACE1005519
Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds
3.3e-55:521:74
Hs.72292:AF024636
- 35 F-PLACE1005539
HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U
5.8e-05:277:63
Hs.103804:AF068846
- 40 F-PLACE1005544
- F-PLACE1005569
EST
0.38:60:75
45 Hs.137086:AA912486
- F-PLACE1005601
Homo Sapiens angiotensin II receptor gene, complete cds
0.016:72:84
50 Hs.20954:AI054441
- F-PLACE1005660
- F-PLACE1005669
55 Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds
3.5e-08:461:60
Hs.113286:U77783

- F-PLACE1005682
- F-PLACE1005725
Huntingtin (Huntington disease)
5 1.1e-06:401:61
Hs.79391:L12392
- F-PLACE1005736
ESTs
10 3.6e-63:343:94
Hs.17757:AA875839
- F-PLACE1005745
ESTs, Weakly similar to HYPOTHETICAL 25.2 KD PROTEIN IN ACB1-KSS1 INTERGENIC REGION [*S.cerevisiae*]
15 6.9e-66:351:94
Hs.7870:AI078137
- F-PLACE1005768
ESTs
20 7.9e-60:318:95
Hs.143856:AI186351
- F-PLACE1005815
Mutated in colorectal cancers
25 0.0029:199:62
Hs.1345:M62397
- F-PLACE1005878
ESTs, Highly similar to CHLORINE CHANNEL PROTEIN P64 [*Bos taurus*]
30 5.0e-38:464:70
Hs.118991:AA675919
- F-PLACE1005927
INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX ACID LABILE CHAIN PRECURSOR
35 0.010:511:59
Hs.839:M86826
- F-PLACE1006071
EST
40 0.68:224:59
Hs.161788:AA371859
- F-PLACE1006073
Homo sapiens mRNA for glucuronyltransferase I, complete cds
45 5.5e-96:464:98
Hs.26492:AB009598
- F-PLACE1006079
Homo sapiens BAC clone RG300E22 from 7q21-q31.1
50 1.5e-18:402:65
Hs.99348:AC004774
- F-PLACE1006093
Homo sapiens mRNA for protein phosphatase 1 (PPP1R6)
55 0.0022:306:59
Hs.106471:Y18206

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- 5 F-PLACE1006208
HOMEODOMAIN/POU DOMAIN PROTEIN RDC-1
0.022:425:57
Hs.74095:L20433
- 10 F-PLACE1006219
ESTs, Moderately similar to similar to thymidine diphosphoglucose 4,6-dehydratase [C.elegans]
1.7e-61:294:100
Hs.153778:AI246000
- 15 F-PLACE1006277
EST
0.42:60:75
Hs.137086:AA912486
- 20 F-PLACE1006290
ESTs, Weakly similar to similar to M. musculus MERS and other AHPC/TSA proteins [C.elegans]
1.3e-51:260:98
Hs.132096:AA314601
- 25 F-PLACE1006443
Homo sapiens PB39 mRNA, complete cds
1.2e-53:553:70
Hs.18910:AF045584
- 30 F-PLACE1006515
Homo sapiens mRNA for KIAA0576 protein, partial cds
1.3e-141:655:99
Hs.14687:AB011148
- 35 F-PLACE1006716
EST
7.2e-12:148:75
Hs.162969:AA677315
- 40 F-PLACE1006786
ESTs
0.0050:125:72
Hs.109156:AA193501
- 45 F-PLACE1006809
ESTs
4.5e-99:477:98
Hs.135208:AI093908
- 50 F-PLACE1006959
ESTs
7.4e-72:381:93
Hs.4963:W29030
- 55 F-PLACE1007028
Homo sapiens p17-Beckwith-Wiedemann region 1 C (BWR1C) mRNA, complete cds
1.8e-18:364:65
Hs.154036:AF035444
- F-PLACE1007040
H.sapiens NF-H gene, exon 1 (and joined CDS)
1.4e-09:501:61

Hs.75735:X15306

F-PLACE1007077
ESTs, Moderately similar to testis-specific TCP20 [H.sapiens]
5 0.88:192:62
Hs.85818:AI216525

F-PLACE1007081
Human plectin (PLEC1) mRNA, complete cds
10 0.079:403:60
Hs.79706:U53204

F-PLACE1007096
YY1 transcription factor
15 0.64:173:64
Hs.97496:M77698

F-PLACE1007296
ER LUMEN PROTEIN RETAINING RECEPTOR 1
20 4.2e-73:542:83
Hs.78040:X55885

F-PLACE1007591
EST
25 0.026:136:64
Hs.130897:AI014389

F-PLACE1007626
Homo sapiens unknown mRNA, complete cds
30 2.6e-105:516:97
Hs.11441:AF047439

F-PLACE1007702
Homo sapiens mRNA for UTF1, complete cds
35 0.033:297:62
Hs.158307:AB011076

F-PLACE1007845
ESTs
40 4.8e-22:158:89
Hs.23445:AA489015

F-PLACE1007881

F-PLACE1007971
ESTs, Weakly similar to K07F5.14 [C.elegans]
45 1.1e-128:599:99
Hs.157918:AA313781

F-PLACE1008282
ESTs, Highly similar to HEME-EGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE [Oryctola-
gus cuniculus]
50 2.4e-65:353:94
Hs.130830:W27380

F-PLACE1008297

F-PLACE1008359

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Human arginine-rich protein (ARP) gene, complete cds
0.020:197:64
Hs.75412:M83751

5 F-PLACE1008469
Homo sapiens PB39 mRNA, complete: cds
5.3e-20:620:60
Hs.18910:AF045584

10 F-PLACE1008549
Homo sapiens E74-like factor 5 (ELF5) mRNA, complete cds
1.8e-145:693:98
Hs.159267:AF049703

15 F-PLACE1008657
VILLIN
2.3e-10:356:61
Hs.3046:X12901

20 F-PLACE1008716
Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds
1.5e-31:191:92
Hs.154844:U15128

25 F-PLACE1008744

F-PLACE1008984
Pregnancy-associated plasma protein A
0.0085:268:60
30 Hs.158229:U28727

F-PLACE1008985
Signal transducer and activator of transcription 5A
0.0047:249:64
35 Hs.14203:U43185

F-PLACE1009067
Human density enhanced phosphatase-1 mRNA, complete cds
2.0e-06:453:60
40 Hs.1177:U10886

F-PLACE1009196

F-PLACE1009279
45 Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds
1.9e-11:327:64
Hs.75111:D87258

F-PLACE1009527
50 Human DNA-binding protein ABP/ZF mRNA, complete cds
6.8e-21:125:96
Hs.86185:U82613

F-PLACE1009546
55 TRANSCRIPTION FACTOR RELB
0.051:248:61
Hs.858:M83221

- 5 F-PLACE1009600
ESTs
1.0:124:64
Hs.52794:W51887
- 10 F-PLACE1009735
ESTs
0.022:387:61
Hs.132253:AI027207
- 15 F-PLACE1009982
- F-PLACE1010011
Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds
1.3e-09:330:66
Hs.143551:AF048693
- 20 F-PLACE1010078
ESTs, Weakly similar to HYPOTHETICAL 25.2 KD PROTEIN IN ACB1-KSS1 INTERGENIC REGION [S.cerevisiae]
8.3e-47:474:72
Hs.13144:T67556
- 25 F-PLACE1010081
Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds
2.2e-151:733:97
Hs.103755:AF027706
- 30 F-PLACE1010251
Homo sapiens Na⁺/H⁺ exchanger regulatory factor 2 (NHERF-2) mRNA, complete cds
0.0037:405:60
Hs.101813:AB016243
- 35 F-PLACE1010445
ESTs
1.7e-45:235:97
Hs.144501:N39767
- 40 F-PLACE1010713
Hydroxysteroid (17-beta) dehydrogenase 3
2.8e-20:447:62
Hs.477:U05659
- 45 F-PLACE1010784
Human protease-activated receptor 3 (PAR3) mRNA, complete cds
0.56:199:59
Hs.159196:U92971
- 50 F-PLACE 1010827
H.sapiens mRNA for transmembrane protein rnp24
2.9e-09:346:64
Hs.75914:X92098
- 55 F-PLACE1010968
ESTs
0.00062:52:98
Hs.119408:T87544

- 5 F-PLACE1011045
Homo sapiens E1-like protein mRNA, complete cds
6.0e-129:595:99
Hs.28190:AF094516
- 10 F-PLACE1011116

F-PLACE1011181
ESTs
1.0:301:58
Hs.80285:AI092519
- 15 F-PLACE1011236
Homo sapiens putative renal organic anion transporter 1 (hROAT1) mRNA, complete cds
1.1e-41:776:62
Hs.23965:AF057039
- 20 F-PLACE1011364
ESTs, Weakly similar to HYPOTHETICAL 141.2 KD PROTEIN EEED8.9 IN CHROMOSOME II [C.elegans]
3.7e-53:276:96
Hs.106499:W28299
- 25 F-PLACE1011407
ESTs, Moderately similar to ZINC FINGER PROTEIN 140 [H.sapiens]
3.2e-15:228:70
Hs.152174:AI199619
- 30 F-PLACE1011516
ESTs, Weakly similar to HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION [S.cerevisiae]
1.7e-85:444:95
Hs.110978:AA843431
- 35 F-PLACE1011708
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds
5.9e-145:722:96
Hs.148318:AF034611
- 40 F-PLACE1011824
Human Ste20-like kinase (MST2) mRNA, complete cds
1.6e-101:561:92
Hs.92317:U26424
- 45 F-PLACE1011978
Homo sapiens DNA from chromosome 19, BAC 33152
3.8e-67:733:72
Hs.55452:AC003973
- 50 F-PLACE2000118
Homo sapiens DNA sequence from PAC 393P12 on chromosome Xp11.21. Contains a hypothetical protein KIAA0413 (KIAA0412, KIAA0065, KIAA0569) LIKE Zinc Finger protein pseudogene, a hypothetical Proline-rich protein KIAA0269 LIKE gene and a 60S Ribosomal Protein L7 LIKE pseudogene. Contains ESTs, an STS and a GSS (BAC end sequence)
7.8e-115:568:95
Hs.120856:AL022578
- 55 F-PLACE2000219
EST

- 8.7e-11:137:75
Hs.98191:AA417044
- 5 F-PLACE3000181
Human protocadherin 42 mRNA, complete cds for abbreviated PC42
1.5e-128:745:90
Hs.79769:L11370
- 10 F-PLACE3000213
EST
1.0:219:63
Hs.98452:AA426058
- 15 F-PLACE4000354
ESTs
1.4e-13:190:71
Hs.138841:R94879
- 20 F-PLACE4000455
- F-SKNMC1000004
Homo sapiens GABA-B receptor mRNA, complete cds
0.00039:275:62
Hs.12307:AF056085
- 25 F-SKNMC1000014
ESTs
3.3e-38:196:98
Hs.113307:H16716
- 30 F-SKNMC1000082
Complement component 4A
0.98:324:63
Hs.76682:K02403
- 35 F-THYRO1000036
Homo sapiens mRNA for putative ATPase, partial
0.98:199:60
Hs.91471:AJ006268
- 40 F-THYRO1000061
Human kinase Myt1 (Myt1) mRNA, complete cds
1.0:210:62
Hs.77783:AF014118
- 45 F-THYRO1000099
ESTs
2.5e-119:605:96
Hs.11782:W07369
- 50 F-THYRO1000196
Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds
1.6e-126:475:98
Hs.115418:AF016272
- 55 F-THYRO1000400
Human R kappa B mRNA, complete cds
0.64:223:63

Hs.95262:U08191

F-THYRO1000580

ESTs, Weakly similar to ZINC FINGER PROTEIN 7 [H.sapiens]

5.4e-27:248:76

Hs.25465:AA528105

F-THYRO1000584

Alpha mannosidase II isozyme

2.2e-06:528:60

Hs.155961:L28821

F-THYRO1000678

Gap junction protein, beta 2, 26kD (connexin 26)

1.3e-33:266:80

Hs.81795:M86849

F-THYRO1000776

Human involucrin mRNA

0.0025:497:59

Hs.157091:M13903

F-THYRO1000795

MITOCHONDRIAL 2-OXOGLUTARATE/MALATE CARRIER PROTEIN

4.1e-19:532:62

Hs.3816:AF070548

F-THYRO1000846

Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds

0.029:387:60

Hs.27910:AF049105

F-THYRO1000866

Homo sapiens SKB1Hs mRNA, complete cds

1.1e-92:529:89

Hs.12912:AF015913

F-THYRO1000956

Homo sapiens mRNA for G-protein coupled receptor

1.8e-15:474:64

Hs.155235:Y13583

F-THYRO1000964

Human OB binding protein-2 (OB-BP2) mRNA, complete cds

0.22:303:61

Hs.117005:U71383

F-THYRO1000999

EST

2.0e-05:198:63

Hs.146520:AI130948

F-THYRO1001063

Human mRNA for cerebroside sulfotransferase, complete cds

0.51:448:60

Hs.17958:D88667

F-THYRO1001071

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- ESTs
2.1e-29:237:83
Hs.155582:AI125241
- 5 F-THYRO1001102
ESTs, Weakly similar to growth arrest inducible gene product [H.sapiens]
4.7e-32:208:88
Hs.7854:W21970
- 10 F-THYRO1001113
Homo sapiens dysferlin mRNA, complete cds
3.2e-53:684:68
Hs.143897:AF075575
- 15 F-THYRO1001128
ESTs
2.1e-120:589:97
Hs.62595:AA306052
- 20 F-THYRO1001205

F-THYRO1001237
ESTs
0.66:326:60
Hs.148352:U80757
- 25 F-THYRO1001242
Protein phosphatase 2C alpha [human, teratocarcinoma, mRNA, 2346 nt]
0.017:188:63
Hs.57764:S87759
- 30 F-THYRO1001266
Human sodium iodide symporter mRNA, complete cds
8.6e-43:806:62
Hs.103983:U66088
- 35 F-THYRO1001327
ESTs
2.8e-50:264:96
Hs.154667:AI343524
- 40 F-THYRO1001456
EST
0.90:84:72
Hs.130049:AA902650
- 45 F-THYRO1001457
Protein kinase C, mu
6.0e-53:705:67
Hs.2891:X75756
- 50 F-THYRO1001471
ESTs
8.0e-52:278:94
Hs.7604:W31115
- 55 F-THYRO1001478
Human mRNA for KIAA0150 gene, partial cds

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- 0.79:150:66
Hs.98508:D63484
- 5 F-THYRO1001495
Homo sapiens KIAA0415 mRNA, complete cds
9.5e-75:550:82
Hs.7289:AB007875
- 10 F-THYRO1001523
ESTs
7.2e-19:142:86
Hs.140588:H60533
- 15 F-THYRO1001529
ESTs
5.7e-24:141:95
Hs.114172:AA703201
- 20 F-THYRO1001593
H.sapiens mRNA for serine/threonine protein kinase EMK
1.4e-70:643:74
Hs.157199:X97630
- 25 F-THYRO1001608
Human mRNA for KIAA0227 gene, partial cds
2.6e-07:533:59
Hs.79170:D86980
- 30 F-THYRO1001641
ESTs
0.87:269:59
Hs.14599:AA522511
- 35 F-THYRO1001700
Homo sapiens c-Jun N-terminal kinase kinase 2 (JNKK2) mRNA, complete cds
3.3e-05:441:59
Hs.110299:AF013589
- 40 F-THYRO1001702
Human plectin (PLEC1) mRNA, complete cds
0.00017:346:62
Hs.79706:U53204
- 45 F-THYRO1001725
Homo sapiens mRNA for procollagen I-N proteinase
1.3e-06:275:64
Hs.120330:AJ003125
- 50 F-THYRO1001770
Homo sapiens mRNA for HsGAK, complete cds
0.046:265:58
Hs.153227:D88435
- 55 F-THYRO1001803
EST
0.0085:201:63
Hs.158782:AI376601

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5 F-Y79AA1000030
ESTs
0.00051:276:60
Hs.111999:AA465020

10 F-Y79AA1000127
ESTs
1.3e-85:430:96
Hs.49932:W58552

15 F-Y79AA1000207
ESTs
4.5e-81:407:96
Hs.125308:AI376737

20 F-Y79AA1000226
ESTs, Highly similar to HYPOTHETICAL 52.8 KD PROTEIN T05E11.5 IN CHROMOSOME IV [Caenorhabditis
elegans]
0.00081:76:84
Hs.11221:AI192291

25 F-Y79AA1000270
Human mRNA for ORF, Xq terminal portion
9.9e-97:590:88
Hs.6551:D16469

30 F-Y79AA1000426
CELL SURFACE GLYCOPROTEIN MUC18 PRECURSOR
0.045:507:59
Hs.82914:X68264

35 F-Y79AA1000521
Homo sapiens mRNA for putative G-protein coupled receptor, EDG6
0.0029:489:58
Hs.159543:AJ000479

40 F-Y79AA1000750
ESTs
9.9e-12:252:65
Hs.52885:H29851

45 F-Y79AA1000776
ESTs
1.4e-50:340:87
Hs.144198:AI017555

50 F-Y79AA1000777
Homo sapiens mRNA for putative transcription factor, partial
3.9e-10:501:61
Hs.26782:AJ009770

55 F-Y79AA1000876
Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds
1.3e-11:323:66
Hs.30250:AF055376

F-Y79AA1000888
Homo sapiens mRNA for KIAA0469 protein, complete cds

- 1.5e-05:641:58
Hs.7764:AB007938
- 5 F-Y79AA1000959
Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds
5.3e-54:277:96
Hs.53066:AF093420
- 10 F-Y79AA1000967
Human mRNA for KIAA0369 gene, complete cds
8.1e-10:517:61
Hs.21355:AB002367
- 15 F-Y79AA1001013
ESTs
2.4e-44:259:93
Hs.109468:W52074
- 20 F-Y79AA1001056
ESTs, Moderately similar to maternal transcript Maid [M.musculus]
4.7e-07:90:87
Hs.36794:AI038407
- 25 F-Y79AA1001062
ESTs, Weakly similar to tumor necrosis factor-alpha-induced protein B12 [H.sapiens]
1.6e-60:320:96
Hs.13982:W27344
- 30 F-Y79AA1001090
H.sapiens DAP-kinase mRNA
2.3e-06:465:59
Hs.153924:X76104
- 35 F-Y79AA1001212
Homo sapiens SL15 protein mRNA, complete cds
1.5e-163:763:98
Hs.6710:AF038961
- 40 F-Y79AA1001264
Homo sapiens mRNA for MSJ-1, complete cds
5.3e-15:367:64
Hs.3845:AB014888
- 45 F-Y79AA1001272
Human plectin (PLEC1) mRNA, complete cds
6.3e-05:325:63
Hs.79706:U53204
- 50 F-Y79AA1001328
Homo sapiens Delta mRNA, complete cds
1.8e-07:271:61
Hs.144631:AF003522
- 55 F-Y79AA1001426
Aldehyde dehydrogenase 7
0.94:485:56
Hs.83155:U10868

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F-Y79AA1001427
 NADH-CYTOCHROME B5 REDUCTASE
 1.7e-56:649:69
 Hs.75666:M28713
 5

F-Y79AA1001430
 Homo sapiens mRNA for KIAA0469 protein, complete cds
 2.8e-124:577:99
 Hs.7764:AB007938
 10

F-Y79AA1001523
 Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds
 1.1e-92:496:93
 Hs.128763:AF009353
 15

F-Y79AA1001530
 Human beta-tubulin gene (5-beta) with ten Alu family members
 1.0e-131:669:95
 Hs.108014:X00734
 20

F-Y79AA1001592
 ESTs
 1.2e-88:212:97
 Hs.131180:AA594251
 25

F-Y79AA1001727
 F-Y79AA1001787
 Human mRNA for KIAA0315 gene, partial cds
 0.48:248:63
 Hs.3989:AB002313
 30

F-Y79AA1001793
 ESTs
 1.4e-67:192:98
 Hs.118559:AA887084
 35

F-Y79AA1001795
 Homo sapiens mRNA for GalT4 protein
 5.3e-89:431:98
 Hs.21495:AL031228
 40

F-Y79AA1001799
 NUCLEAR FACTOR RIP140
 0.54:182:62
 Hs.155017:X84373
 45

F-Y79AA1001803
 ESTs, Highly similar to MELANOMA-ASSOCIATED ANTIGEN XP [Homo sapiens]
 0.72:169:63
 Hs.94011:AA627644
 50

F-Y79AA1001863
 EST
 1.0:114:63
 Hs.152260:AA489703
 55

F-Y79AA1002022

B94 PROTEIN
5.7e-13:469:65
Hs.75522:M92357

5 F-Y79AA1002058
Homo sapiens clone 24733 mRNA sequence
1.7e-154:740:98
Hs.21970:AF052149

10 F-Y79AA1002121
EST
0.14:104:66
Hs.100070:M91493

15 F-Y79AA1002129
ESTs
5.1e-90:431:98
Hs.40719:AI183452

20 F-Y79AA1002213

F-Y79AA1002334
ESTs
5.0e-20:187:80
25 Hs.111900:AA397579

F-Y79AA1002373
ESTs
4.5e-37:192:98
30 Hs.118559:AA887084

F-Y79AA1002376
Homo sapiens cytoplasmic dynein intermediate chain 1 mRNA, complete cds
1.2e-36:657:64
35 Hs.65248:AF063228

F-Y79AA1002378
Homo sapiens KIAA0426 mRNA, complete cds
4.9e-38:424:72
40 Hs.97476:AB007886

F-Y79AA1002381
CELL DIVISION PROTEIN KINASE 3
8.4e-17:580:61
45 Hs.100009:X66357

Homology search result 9

50 [0302] The result of the homology search in the Human Unigene(<http://www.ncbi.nlm.nih.gov/UniGene>) using the
clone sequences of the 3'-ends.

Indicated are from the top,
the name of the clone sequence,
title of the top hit data,
55 the P-value: the length of the sequence used for comparison (nucleotide):similarity (%),
the Accession No. of the top hit data.

[0303] Blank indicates that the 3'-end sequence corresponding to the 5'-end was not determined in the clone.

[0304] Data were not shown for the clones in which the P-value was higher than 1.

5	R-HEMBA1000006 ESTs 1.0:85:71 Hs.130699:AA621478
10	R-HEMBA1000121 ESTs 1.3e-111:545:97 Hs.153432:AA098922
15	R-HEMBA1000128 ESTs, Weakly similar to HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-MRPL8 INTERGENIC REGION PRE-CURSOR [S.cerevisiae] 3.0e-98:532:93 Hs.7745:H92988
20	R-HEMBA1000275 ESTs 6.5e-11:81:81 Hs.163492:AI334460
25	R-HEMBA1000300 Homo sapiens mRNA for putative lipoic acid synthetase, partial 1.2e-39:309:81 Hs.53531:AJ224162
30	R-nnnnnnnnnnnnn ESTs 4.9e-95:455:98 Hs.154009:AI284184
35	R-HEMBA1000462 Homo sapiens clone 243 unknown mRNA, complete sequence 3.6e-91:313:94 Hs.20423:AF091094
40	R-HEMBA1000477 ESTs 4.7e-111:541:97 Hs.84526:AI341541
45	R-HEMBA1000590 Homo sapiens mRNA for matrilin-4, partial 2.6e-102:547:93 Hs.129361:AJ007581
50	R-HEMBA1000634 ESTs 0.85:189:62 Hs.131268:AA909162
55	R-HEMBA1000671 ESTs 6.5e-84:432:96 Hs.31991:T78668

5 R-HEMBA1000713
Homo sapiens 10kD protein (BC10) mRNA, complete cds
4.0e-119:575:97
Hs.5300:AF053470

10 R-HEMBA1000732
EST
3.9e-81:435:92
Hs.146718:AI146722

15 R-HEMBA1000875
EST
0.023:207:62
Hs.148275:AA907849

20 R-HEMBA1000940
Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds
7.4e-31:211:81
Hs.97203:U83171

25 R-HEMBA1000962
ESTs
1.1e-104:515:97
Hs.8978:W63573

30 R-HEMBA1001184
EST
7.1e-07:382:62
Hs.124559:AA847550

35 R-HEMBA1001221
ESTs, Weakly similar to transmembrane protein [H.sapiens]
1.2e-95:487:95
Hs.22791:AI056665

40 R-HEMBA1001228
Human germline oligomeric matrix protein (COMP) mRNA, complete cds
4.0e-42:170:92
Hs.1584:AC003107

45 R-HEMBA1001272
ESTs
5.7e-71:514:84
Hs.26966:N74056

50 R-HEMBA1001296
EST
1.7e-93:494:95
Hs.102465:N27272

55 R-HEMBA1001297
Homo sapiens putative transcription factor CA150 mRNA, complete cds
1.5e-93:466:96
Hs.13063:AF017789

R-HEMBA1001390

- ESTs
1.6e-42:181:89
Hs.139190:N55515
- 5 R-HEMBA1001563
Homo sapiens DEC-205 mRNA, complete cds
8.4e-42:311:83
Hs.153563:AF011333
- 10 R-HEMBA1001621
ESTs, Highly similar to PROBABLE G PROTEIN-COUPLED RECEPTOR APJ [Homo sapiens]
4.2e-56:386:86
Hs.9305:W84893
- 15 R-HEMBA1001878
Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds
1.1e-80:433:93
Hs.10290:AF090988
- 20 R-HEMBA1001886
Zinc finger protein 141 (clone pHZ-44)
5.9e-61:530:80
Hs.159596:L15309
- 25 R-HEMBA1002048
ESTs
0.95:127:63
Hs.98690:AA431162
- 30 R-HEMBA1002131

R-HEMBA1002163
ESTs, Weakly similar to K09E9.2 [C.elegans]
5.9e-36:225:90
- 35 Hs.26813:AI339473

R-HEMBA1002167
ESTs
1.5e-35:325:80
- 40 Hs.124171:N98933

R-HEMBA1002178
MICROSOMAL DIPEPTIDASE PRECURSOR
0.99:243:61
- 45 Hs.109:J05257

R-HEMBA1002195
Deoxyhypusine synthase
1.9e-19:109:100
- 50 Hs.79064:U79262

R-HEMBA1002227
Myristoylated alanine-rich C-kinase substrate
2.0e-116:567:97
- 55 Hs.75607:D10522

R-HEMBA1002316
Homo sapiens mRNA for putative GTP-binding protein

- 8.2e-20:160:85
Hs.101033:Y14391
- 5 R-HEMBA1002420
ESTs, Weakly similar to T03G11.6 gene product [C.elegans]
2.7e-78:402:97
Hs.108354:W19984
- 10 R-HEMBA1002421
Syndecan 2 (heparan sulfate proteoglycan 1, cell surface-associated, fibroglycan)
1.9e-91:443:97
Hs.1501:J04621
- 15 R-HEMBA1002524
Human MHC Class I region proline rich protein mRNA, complete cds
1.0e-111:551:96
Hs.41548:U63336
- 20 R-HEMBA1002551
ESTs
3.4e-107:553:96
Hs.92071:W80592
- 25 R-HEMBA1002767
Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds
5.5e-108:568:95
Hs.19154:AF038660
- 30 R-HEMBA1002985
ESTs
4.4e-39:211:96
Hs.126894:AA932538
- 35 R-HEMBA1003047
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds
1.6e-115:571:96
Hs.148318:AF034611
- 40 R-HEMBA1003072
EST
0.044:220:61
Hs.136349:AA490873
- 45 R-HEMBA1003101
Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds
1.2e-117:575:97
Hs.26350:AF049891
- 50 R-HEMBA1003120
Zinc finger protein 10 (KOX 1)
5.8e-41:412:73
Hs.2479:X78933
- 55 R-HEMBA1003230
Homo sapiens UP50 mRNA, complete cds
4.2e-44:258:93
Hs.11494:AF093118

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5 R-HEMBA1003294
ESTs
4.3e-84:410:98
Hs.113517:AA418756

10 R-HEMBA1003315
ESTs, Weakly similar to TIP49 [R.norvegicus]
7.3e-73:476:87
Hs.6455:AA515838

15 R-HEMBA1003392
Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds
8.3e-117:557:98
Hs.23672:AF074264

20 R-HEMBA1003399
ESTs, Highly similar to MVP1 PROTEIN [Saccharomyces cerevisiae]
8.0e-94:526:92
Hs.12169:N38744

25 R-HEMBA1003487
ESTs
4.5e-84:417:96
Hs.21835:AA458524

30 R-HEMBA1003497
ESTs
1.4e-72:346:99
Hs.129837:AA778570

35 R-HEMBA1003530
ESTs
8.5e-82:459:91
Hs.22140:R41751

40 R-HEMBA1003602
ESTs
1.0e-101:592:90
Hs.124342:AA829829

45 R-HEMBA1003732
ESTs
2.1e-111:530:99
Hs.101660:AA481200

50 R-HEMBA1003945
Calcineurin B
2.9e-83:410:97
Hs.1335:M30773

55 R-HEMBA1004007
Homo sapiens PYRIN (MEFV) mRNA, complete cds
3.8e-57:382:77
Hs.113283:AF018080

R-HEMBA1004085
ESTs
3.0e-59:396:87

Hs.102480:AA520980

R-nnnnnnnnnnnnn
Homo sapiens intersectin short form mRNA, complete cds
5 2.0e-116:569:97
Hs.66392:AF064244

R-HEMBA1004250
ESTs
10 1.6e-97:469:97
Hs.125529:AA883986

R-HEMBA1004391
EST
15 0.085:113:63
Hs.157582:AI356856

R-HEMBA1004444
ESTs
20 2.3e-88:430:98
Hs.141680:N98441

R-HEMBA1004454
ESTs
25 1.7e-71:338:100
Hs.103913:AA740543

R-HEMBA1004505
ESTs
30 2.2e-63:329:95
Hs.4814:AA631254

R-HEMBA1004785
EST
35 1.0:77:67
Hs.144066:AA905236

R-HEMBA1004797
ESTs
40 4.1e-11:71:100
Hs.27206:AA626782

R-HEMBA1004952
ESTs
45 6.0e-93:435:99
Hs.115120:AA935633

R-HEMBA1004971
ESTs
50 0.98:152:58
Hs.112621:AA608964

R-HEMBA1004982
ESTs
55 2.3e-109:516:98
Hs.14877:AA749081

R-HEMBA1005070

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Human mRNA for KIAA0310 gene, complete cds
4.0e-96:381:91
Hs.5716:AB002308

5 R-HEMBA1005084
ESTs
1.0:75:80
Hs.62119:AA043299

10 R-HEMBA1005145
Homo sapiens LIM protein mRNA, complete cds
1.6e-58:278:84
Hs.154103:AF061258

15 R-HEMBA1005230
ESTs
3.7e-65:336:95
Hs.124946:AI026708

20 R-HEMBA1005246

R-HEMBA1005267
Human protein immuno-reactive with anti-PTH polyclonal antibodies mRNA, partial cds
7.8e-75:536:81
25 Hs.44566:U28831

R-HEMBA1005337
EST
8.7e-58:291:97
30 Hs.48956:N64339

R-HEMBA1005430
ESTs
7.6e-83:388:100
35 Hs.28968:AA524690

R-HEMBA1005449
ESTs
5.0e-47:317:86
40 Hs.23650:H21144

R-HEMBA1005489
ESTs
1.8e-96:504:94
45 Hs.8028:AA053817

R-HEMBA1005522
EST
1.0:98:64
50 Hs.157385:AI364194

R-HEMBA1005545
MUSCARINIC ACETYLCHOLINE RECEPTOR M3
6.3e-117:579:96
55 Hs.7138:U29589

R-HEMBA1005698
ESTs

- 1.6e-113:562:96
Hs.12942:AI042353
- 5 R-HEMBA1005913
ESTs
2.8e-109:564:94
Hs.28827:AI125541
- 10 R-HEMBA1005929
Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds
9.6e-63:497:77
Hs.97203:U83171
- 15 R-HEMBA1005945
ESTs
1.1e-74:412:92
Hs.32246:AA464020
- 20 R-HEMBA1006016
ESTs
1.4e-18:162:82
Hs.149448:AI082465
- 25 R-HEMBA1006171
EST
0.049:94:69
Hs.159919:AA961766
- 30 R-HEMBA1006276
ESTs
6.3e-22:257:75
Hs.138847:N64493
- 35 R-HEMBA1006299
ESTs, Weakly similar to R06B9.b [C.elegans]
3.9e-107:596:91
Hs.30432:W28988
- 40 R-HEMBA1006311
Homo sapiens SALL1 gene, partial
0.99:273:60
Hs.123094:X98833
- 45 R-HEMBA1006335
ESTs
2.5e-72:447:89
Hs.23579:W38893
- 50 R-HEMBA1006357
ESTs
6.3e-15:187:74
Hs.161714:AA229078
- 55 R-HEMBA1006430
Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds
2.9e-47:303:88
Hs.129708:AF064090

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R-HEMBA1006482
 Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds
 5.5e-107:537:96
 Hs.14511:AF026852
 5

R-HEMBA1006517
 ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
 2.7e-43:173:86
 Hs.141505:N30650
 10

R-HEMBA1006544
 Homo sapiens mRNA for small GTP-binding protein, complete cds
 5.8e-60:329:80
 Hs.115325:D84488
 15

R-HEMBA1006572
 ESTs
 7.2e-94:450:99
 Hs.123933:AA758566
 20

R-HEMBA1006658
 Homo sapiens mRNA for KIAA0687 protein, partial cds
 2.3e-112:570:94
 Hs.3628:AB014587
 25

R-HEMBA1006707
 Homo sapiens mRNA for matrilin-4, partial
 1.7e-79:389:97
 Hs.129361:AJ007581
 30

R-HEMBA1006724
 R-HEMBA1006749
 Homo sapiens mRNA for matrilin-4, partial
 1.0e-89:472:94
 Hs.129361:AJ007581
 35

R-HEMBA1006770
 ESTs, Moderately similar to CAGH4 [H.sapiens]
 2.0e-112:554:96
 Hs.41641:AA428519
 40

R-HEMBA1006902
 Homo sapiens mRNA for matrilin-4, partial
 3.0e-113:540:98
 Hs.129361:AJ007581
 45

R-HEMBA1006912
 H.sapiens mRNA for phosphoinositide 3-kinase
 5.9e-45:297:86
 Hs.101238:Y11312
 50

R-HEMBA1006916
 Homo sapiens Grb14 mRNA, complete cds
 5.8e-116:346:99
 Hs.83070:L76687
 55

R-HEMBA1006960

ESTs
1.7e-110:519:99
Hs.22015:AI359551

5 R-HEMBA1007013
ESTs
0.53:280:59
Hs.143532:AI087321

10 R-HEMBA1007057

R-HEMBA1007063
EST
3.2e-41:310:83

15 Hs.163333:AA879053

R-HEMBA1007241
ESTs
1.8e-103:492:98

20 Hs.127478:AI188768

R-HEMBA1007291
Human mRNA for KIAA0266 gene, complete cds
8.7e-46:283:89

25 Hs.78878:D87455

R-HEMBA1007332
ESTs, Weakly similar to hTAFII100 [H.sapiens]
2.8e-17:161:80

30 Hs.3727:AA205887

R-HEMBA1000106
ESTs
1.3e-100:491:97

35 Hs.27774:AA576731

R-HEMBA1000276

R-HEMBA1000309
EST
1.0:150:64

40 Hs.125409:AA879096

R-HEMBA1000407
ESTs, Weakly similar to C47D12.2 [C.elegans]
4.1e-110:535:97

45 Hs.14328:AA503393

R-HEMBA1000447
Homo sapiens JWA protein mRNA, complete cds
5.6e-109:533:97

50 Hs.92384:AF070523

R-HEMBA1000542
ESTs, Weakly similar to C01H6.7 [C.elegans]
1.6e-88:497:91

55 Hs.18171:AA524327

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5 R-HEMBB1000567
 Insulin-like growth factor 2 (somatomedin A)
 8.9e-61:369:88
 Hs.155487:J03242

 10 R-HEMBB1000642
 ESTs
 2.2e-44:308:84
 Hs.141318:N71080

 15 R-HEMBB1000668
 ESTs, Weakly similar to hTAFII100 [H.sapiens]
 2.5e-102:520:95
 Hs.3830:AA167691

 20 R-HEMBB1000679
 ESTs
 6.7e-36:188:97
 Hs.154218:AA169554

 25 R-HEMBB1000881
 ESTs
 8.4e-105:519:96
 Hs.110967:AA570505

 30 R-HEMBB1000905
 ESTs
 1.1e-94:454:98
 Hs.52515:AA464314

 35 R-HEMBB1001026
 ESTs
 0.22:93:69
 Hs.119510:AA630235

 40 R-HEMBB1001048
 EST
 0.42:127:66
 Hs.147466:AI215091

 45 R-HEMBB1001200
 ESTs
 3.7e-07:330:62
 Hs.10109:AI148628

 50 R-HEMBB1001407
 MHC class II transactivator
 3.8e-35:414:71
 Hs.3076:U18259

 55 R-HEMBB1001530
 ESTs
 2.4e-95:455:98
 Hs.8956:AI146421

 R-HEMBB1001547
 ESTs
 1.0e-111:533:98

- Hs.33979:AI074147
- R-HEMBB1001573
ESTs, Moderately similar to LL5 protein [R.norvegicus]
5 1.7e-06:64:95
Hs.131327:AI148746
- R-HEMBB1001847
ESTs
10 1.4e-54:280:96
Hs.109755:AA180809
- R-HEMBB1001959
Homo sapiens clone 24781 mRNA sequence
15 1.5e-104:504:97
Hs.108112:AF070640
- R-HEMBB1001978
Homo sapiens mRNA for TRAF5, complete cds
20 7.0e-28:220:84
Hs.29736:AB000509
- R-HEMBB1002039
ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
25 1.5e-34:423:72
Hs.154912:N63897
- R-HEMBB1002041
ESTs, Weakly similar to transmembrane protein [H.sapiens]
30 7.0e-122:575:98
Hs.22791:AI056665
- R-HEMBB1002051
ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis
35 elegans]
4.2e-43:298:84
Hs.141429:AA631915
- R-HEMBB1002120
ESTs
40 1.4e-91:438:99
Hs.145014:AI218562
- R-HEMBB1002162
ESTs
45 1.0e-34:238:86
Hs.164036:AA845659
- R-HEMBB1002228
Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds
50 1.7e-59:583:77
Hs.129735:AF010144
- R-HEMBB1002245
ESTs
55 9.1e-66:383:91
Hs.8989:R71365

R-HEMBB1002302
 ESTs
 3.6e-54:329:89
 Hs.37706:AA005120
 5

R-HEMBB1002427
 ESTs
 4.2e-83:400:98
 Hs.130783:AI263114
 10

R-HEMBB1002465
 EST
 9.9e-38:231:90
 Hs.133443:AI061405
 15

R-HEMBB1002661
 ESTs
 2.5e-101:472:99
 Hs.26878:AI421289
 20

R-HEMBB1002663
 Small inducible cytokine A5 (RANTES)
 7.1e-43:268:88
 Hs.155464:AF088219
 25

R-HEMBB1002693
 ESTs
 4.6e-84:435:96
 Hs.155522:AA829725
 30

R-MAMMA1000046
 EST
 3.9e-06:196:65
 Hs.136664:AA707467
 35

R-MAMMA1000102
 Human G protein-coupled receptor (STRL22) mRNA, complete cds
 1.1e-31:237:83
 Hs.46468:U45984
 40

R-MAMMA1000106
 ESTs
 1.3e-65:333:95
 Hs.130749:AI284219
 45

R-MAMMA1000118
 ESTs
 7.3e-95:465:97
 Hs.119286:AA126730
 50

R-MAMMA1000141
 ESTs
 4.2e-94:515:93
 Hs.8116:H23508
 55

R-MAMMA1000204
 Homo sapiens dysferlin mRNA, complete cds
 2.3e-108:542:96

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Hs.143897:AF075575

R-MAMMA1000226
ESTs
5 2.1e-112:535:98
Hs.105761:AA903862

R-MAMMA1000403
ESTs
10 1.5e-36:162:83
Hs.152413:AA780515

R-MAMMA1000449
EST
15 1.5e-40:347:78
Hs.163333:AA879053

R-MAMMA1000457
Homo sapiens clone 638 unknown mRNA, complete sequence
20 2.6e-117:570:97
Hs.5825:AF091084

R-MAMMA1000473
ESTs
25 1.3e-62:308:99
Hs.53565:W02102

R-MAMMA1000496
Phosphodiesterase 4C, cAMP-specific (dunce (Drosophila)-homolog phosphodiesterase E1)
30 0.051:125:68
Hs.189:AC005759

R-MAMMA1000528
ESTs
35 2.4e-12:216:71
Hs.134105:AI078038

R-MAMMA1000591
ESTs
40 5.0e-104:509:98
Hs.151678:AA032243

R-MAMMA1000614
Homo sapiens mRNA for KIAA0665 protein, complete cds
45 0.57:251:62
Hs.119004:AB014565

R-MAMMA1000652
ESTs
50 0.93:49:87
Hs.13248:R54144

R-MAMMA1000681
ESTs
55 1.3e-87:434:97
Hs.46668:N47089

R-MAMMA1000706

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Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds
3.7e-48:232:100
Hs.18953:AF067223

5 R-MAMMA1000788
ESTs
3.7e-108:559:94
Hs.38969:AA130220

10 R-MAMMA1000810
ESTs
1.2e-45:347:80
Hs.146811:AA410788

15 R-MAMMA1000814
ESTs
1.1e-18:288:70
Hs.140608:N53448

20 R-MAMMA1000881
ESTs
1.9e-107:557:96
Hs.141602:N63562

25 R-MAMMA1000986
ESTs
3.8e-46:342:83
Hs.132722:AA618531

30 R-MAMMA1000994
Homo sapiens mRNA for ISLR, complete cds
1.2e-109:552:96
Hs.102171:AB003184

35 R-MAMMA1001043
ESTs
2.3e-88:445:96
Hs.20450:AI094818

40 R-MAMMA1001066
Homo sapiens KIAA0414 mRNA, partial cds
1.5e-43:282:81
Hs.127649:AB007874

45 R-MAMMA1001094
Homo sapiens clone 243 unknown mRNA, complete sequence
3.0e-116:566:97
Hs.20423:AF091094

50 R-MAMMA1001141
ESTs
1.2e-104:496:98
Hs.29669:AI285856

55 R-MAMMA1001150
ESTs, Highly similar to MYOSIN LIGHT CHAIN KINASE [Dictyostelium discoideum]
1.9e-59:284:100
Hs.9915:AI300083

5
R-MAMMA1001237
ESTs
0.45:206:62
Hs.121366:AA758653

10
R-MAMMA1001284
ESTs
6.3e-40:279:85
Hs.109765:AI096738

15
R-MAMMA1001310
ESTs, Moderately similar to !!!! ALU SUBFAMTLY J WARNING ENTRY !!!! [H.sapiens]
5.1e-98:498:96
Hs.27264:AA159597

20
R-MAMMA1001418
Human mRNA for platelet-activating factor acetylhydrolase 2, complete cds
1.2e-41:302:85
Hs.86188:D87845

25
R-MAMMA1001532
ESTs
3.9e-22:331:71
Hs.141840:AA028117

30
R-MAMMA1001609
Small inducible cytokine A5 (RANTES)
1.5e-31:277:78
Hs.155464:AF088219

35
R-MAMMA1001615
ESTs
1.1e-72:376:95
Hs.135569:AA923461

40
R-MAMMA1001623
ESTs
7.9e-106:505:98
Hs.22908:AI224910

45
R-MAMMA1001634
Homo sapiens PYRIN (MEFV) mRNA, complete cds
1.9e-44:428:76
Hs.113283:AF018080

50
R-MAMMA1001893
ESTs
8.0e-67:367:92
Hs.19210:W26097

55
R-MAMMA1001901
Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492
4.7e-35:342:69
Hs.127338:AB007961

R-MAMMA1001957
Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2
5.5e-47:383:79

- Hs.1361:M55053
- R-MAMMA1001978
ESTs
5 6.6e-108:560:95
Hs.8859:AA191552
- R-MAMMA1002070
- 10 R-MAMMA1002080
ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]
9.8e-105:542:94
Hs.10092:AI189282
- 15 R-MAMMA1002087
ESTs
4.0e-19:153:84
Hs.136678:AA730474
- 20 R-MAMMA1002095
ESTs
6.8e-34:196:93
Hs.48119:AA454227
- 25 R-MAMMA1002128
ESTs, Highly similar to ABC1 PROTEIN PRECURSOR [Saccharomyces cerevisiae]
9.0e-96:503:94
Hs.39088:AA194773
- 30 R-MAMMA1002142
ESTs
5.6e-21:145:90
Hs.62119:AA043299
- 35 R-MAMMA1002165
ESTs
1.6e-35:351:76
Hs.140413:N47721
- 40 R-MAMMA1002205
Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds
6.4e-42:217:79
Hs.133089:AF064019
- 45 R-MAMMA1002224
ESTs
0.50:170:64
Hs.144140:H04293
- 50 R-MAMMA1002234
- R-MAMMA1002586
ESTs
5.0e-105:529:96
55 Hs.4814:AA631254
- R-MAMMA1002633
ESTs

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7.3e-97:470:98
Hs.38039:AI360128

5 R-MAMMA1003126
ESTs
6.1e-114:567:97
Hs.20733:AI417917

10 R-NT2RM4000100
ESTs
3.6e-71:343:99
Hs.92186:AI080282

15 R-NT2RM4000115
ESTs
1.5e-86:405:100
Hs.129151:AA988192

20 R-NT2RM4000198
ESTs
8.4e-83:462:93
Hs.96772:AI369496

25 R-NT2RM4000284
Human IgG Fc receptor hFcRn mRNA, complete cds
5.4e-95:440:100
Hs.110804:U12255

30 R-NT2RM4000295
ESTs
1.1e-112:544:97
Hs.21452:AA581881

35 R-NT2RM4000326
EST
4.0e-59:301:96
Hs.86264:AA206496

40 R-NT2RM4000417
ESTs
2.0e-88:489:93
Hs.29098:AA521439

45 R-NT2RM4000444
ESTs
6.4e-90:497:92
Hs.6129:U66676

50 R-NT2RM4000587
ESTs
1.0e-97:473:98
Hs.24947:AA039350

55 R-NT2RM4000593
ESTs
9.8e-109:554:95
Hs.7579:AA775865

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- 5 R-NT2RM4000648
ESTs, Moderately similar to GLYPICAN-1 PRECURSOR [Homo sapiens]
7.6e-39:262:85
Hs.118407:AA001322
- 10 R-NT2RM4000761
ESTs
6.4e-86:433:95
Hs.153428:AI246519
- 15 R-NT2RM4000965
ESTs
2.8e-102:523:96
Hs.61790:AA421156
- 20 R-NT2RM4000997
- R-NT2RM4001321
ESTs
2.4e-66:315:100
Hs.75425:AA149434
- 25 R-NT2RM4001325
ESTs
0.99:104:62
Hs.116257:AA628680
- 30 R-NT2RM4001377
Homo sapiens mRNA for KIAA0638 protein, partial cds
9.3e-113:553:96
Hs.77864:AB014538
- 35 R-NT2RM4001735
Homo sapiens clone 23904 mRNA sequence
1.5e-107:553:94
Hs.67364:AF052129
- 40 R-NT2RM4001768
EST
1.6e-14:82:85
Hs.140922:R51520
- 45 R-NT2RM4001843
ESTs
2.1e-123:579:98
Hs.3741:AI057614
- 50 R-NT2RM4002352
Homo sapiens hLRp105 mRNA for LI(L receptor related protein 105, complete cds
1.8e-109:557:95
Hs.143641:AB009462
- 55 R-NT2RP2000092
ESTs
3.3e-08:286:65
Hs.79881:AA401302
- R-NT2RP2000178

ESTs, Weakly similar to MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]
2.3e-95:462:98
Hs.47305:AA195153

5 R-NT2RP2000240
ESTs
1.3e-55:272:98
Hs.125522:AI299693

10 R-NT2RP2000394
ESTs
2.4e-107:528:96
Hs.28555:W55892

15 R-NT2RP2000447
ESTs, Moderately similar to dynamin, internal form 2, short C-terminal form [H.sapiens]
1.6e-67:357:94
Hs.128788:AA424076

20 R-NT2RP2000479
ESTs
2.6e-48:312:86
Hs.146811:AA410788

25 R-NT2RP2000514
EST
3.2e-63:348:93
Hs.44542:N33966

30 R-NT2RP2000533
ESTs
0.017:307:57
Hs.97873:AA402799

35 R-NT2RP2000616
ESTs
1.0e-91:475:95
Hs.50344:AI300539

40 R-NT2RP2000649
Homo sapiens mRNA for Hs Ste24p, complete cds
1.4e-66:322:98
Hs.25846:AB016068

45 R-NT2RP2000663
ESTs
8.2e-59:311:96
Hs.9728:T98746

50 R-NT2RP2000712
EST
1.7e-27:239:76
Hs.161561:W60681

55 R-NT2RP2000739
ESTs, Weakly similar to zinc finger protein [H.sapiens]
6.3e-86:462:93
Hs.13323:AA897542

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- 5 R-NT2RP2000818
ESTs
7.3e-99:485:97
Hs.100525:AI310204
- 10 R-NT2RP2000903
H.sapiens 5T4 gene for 5T4 Oncofetal antigen
1.2e-100:505:96
Hs.82128:AJ012159
- 15 R-NT2RP2001200
Homo sapiens mRNA for KIAA0676 protein, partial cds
6.6e-59:306:95
Hs.115763:AB014576
- 20 R-NT2RP2001223
ESTs
1.2e-94:475:95
Hs.27556:AA115361
- 25 R-NT2RP2001276
ESTs, Moderately similar to regulatory protein [M.musculus]
4.7e-65:354:92
Hs.105547:AI361036
- 30 R-NT2RP2001388
ESTs
5.5e-83:459:93
Hs.15713:AA485755
- 35 R-NT2RP2001469
ESTs, Weakly similar to teg292 protein [M.musculus]
2.0e-30:233:83
Hs.68791:AA527270
- 40 R-NT2RP2001480
Homo sapiens thrombospondin 3 (THBS3) gene, complete cds
2.1e-84:426:95
Hs.82165:L38969
- 45 R-NT2RP2001495
ESTs, Weakly similar to transporter protein [H.sapiens]
1.7e-14:130:84
Hs.18272:N78499
- 50 R-NT2RP2001514
ESTs, Weakly similar to PROBABLE CATION-TRANSPORTING ATPASE YEL031W [Saccharomyces cerevisiae]
3.3e-45:242:95
Hs.9275:AA973284
- 55 R-NT2RP2001538
EST
1.4e-05:111:73
Hs.137268:T39311
- R-NT2RP2001562
EST
0.50:35:91

Hs.140505:AA804211

R-NT2RP2001662

Homo sapiens clone 24615 mRNA sequence

1.0e-95:485:95

Hs.94785:AF055012

R-NT2RP2001755

Homo sapiens mRNA for KIAA0762 protein, partial cds

4.2e-105:576:92

Hs.5378:AB018305

R-NT2RP2001769

ESTs

4.2e-102:548:93

Hs.14014:AA745592

R-NT2RP2001817

ESTs

6.0e-97:472:97

Hs.31176:AI037953

R-NT2RP2001878

ESTs

3.3e-94:475:95

Hs.144655:AI279798

R-NT2RP2001903

ESTs

1.7e-88:461:95

Hs.112218:AI038601

R-NT2RP2001915

ESTs

7.8e-96:480:96

Hs.100890:AA779892

R-NT2RP2001921

ESTs

2.5e-88:466:94

Hs.104859:AA779101

R-NT2RP2001948

ESTs

1.9e-81:439:91

Hs.105463:AA583017

R-NT2RP2001956

ESTs

8.7e-85:477:91

Hs.12101:AA677423

R-NT2RP2002015

ESTs

3.5e-85:431:95

Hs.75425:AA149434

R-NT2RP2002063

Hs.136259:AA347883

R-NT2RP2002942
ESTs
5 9.2e-82:422:96
Hs.140952:R59211

R-NT2RP2002974
ESTs
10 5.6e-99:507:96
Hs.43314:AA160543

R-NT2RP2002976
ESTs
15 2.9e-78:397:91
Hs.83575:N28730

R-NT2RP2003042
ESTs
20 2.7e-107:526:97
Hs.6770:AA972732

R-NT2RP2003179
ESTs
25 2.9e-59:335:92
Hs.87019:AA760977

R-NT2RP2003210
ESTs
30 2.1e-80:419:94
Hs.25354:N28667

R-NT2RP2003302
ESTs, Moderately similar to ZINC FINGER PROTEIN 7 [Homo sapiens]
35 2.1e-92:443:98
Hs.112508:AA599140

R-NT2RP2003369
ESTs
40 9.7e-84:462:92
Hs.155116:C16874

R-NT2RP2003383
Homo sapiens mRNA for KIAA0458 protein, complete cds
45 1.3e-112:549:97
Hs.7414:AB007927

R-NT2RP2003390
Homo sapiens SEC63 (SEC63) mRNA, complete cds
50 4.9e-56:286:96
Hs.31575:AF100141

R-NT2RP2003469
Human mRNA for KIAA0355 gene, complete cds
55 6.6e-40:302:83
Hs.153014:AB002353

R-NT2RP2003545

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- ESTs
8.0e-121:572:98
Hs.23643:AI299952
- 5 R-NT2RP2003593
EST
1.0:124:62
Hs.59890:AA001879
- 10 R-NT2RP2003599
EST
5.2e-06:319:60
Hs.147887:AI223203
- 15 R-NT2RP2003655
ESTs
9.3e-107:519:97
Hs.5831:AA176450
- 20 R-NT2RP2003664
Homo sapiens mRNA for leptin receptor gene-related protein
5.3e-112:549:96
Hs.23581:Y12670
- 25 R-NT2RP2003931
Human mRNA for KIAA0365 gene, partial cds
1.7e-113:571:96
Hs.84123:AB002363
- 30 R-NT2RP2003940
EST
3.0e-71:385:93
Hs.162657:AA603590
- 35 R-NT2RP2003950
Homo sapiens clone 24778 unknown mRNA
5.0e-98:494:95
Hs.25306:AF070572
- 40 R-NT2RP2004069
Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end
6.3e-54:556:74
Hs.103948:K00627
- 45 R-NT2RP2004108
ESTs, Moderately similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]
6.9e-92:442:98
Hs.14831:AI261191
- 50 R-NT2RP2004141
ESTs
8.3e-29:171:93
Hs.25700:AI338437
- 55 R-NT2RP2004179
ESTs
3.1e-71:461:88
Hs.6748:R68509

5 R-NT2RP2004205
ESTs
2.6e-44:397:78
Hs.95115:AA206594

10 R-NT2RP2004447
ESTs
4.0e-101:494:97
Hs.51655:AA523276

15 R-NT2RP2004495
ESTs, Weakly similar to transporter protein [H.sapiens]
6.1e-71:417:92
Hs.18272:N78499

20 R-NT2RP2004524
ESTs
1.8e-93:482:95
Hs.119285:AI225008

25 R-NT2RP2004556
Homo sapiens mRNA for KIAA0459 protein, partial cds
8.8e-48:353:82
Hs.28169:AB007928

30 R-NT2RP2004606
Tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor)
3.5e-116:576:96
Hs.148726:X03124

35 R-NT2RP2004648
ESTs
5.9e-114:600:93
Hs.3741:AI057614

40 R-NT2RP2004670
ESTs
1.7e-92:488:94
Hs.6262:T89093

45 R-NT2RP2004794
EST
0.44:205:57
Hs.147759:AI220726

50 R-NT2RP2004837
ESTs
6.9e-111:576:94
Hs.12305:AA166889

55 R-NT2RP2004847
ESTs
8.3e-94:445:99
Hs.53996:AI268861

R-NT2RP2005027
GLUCOSE TRANSPORTER TYPE 3, BRAIN
2.5e-104:508:97

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	Hs.7594:M20681
	R-NT2RP2005069
	ESTs, Highly similar to vacuolar protein sorting homolog r-vps33b [R.norvegicus]
5	4.7e-111:541:97
	Hs.26510:AA700425
	R-NT2RP2005163
	ESTs
10	6.8e-64:327:89
	Hs.83575:N28730
	R-NT2RP2005181
	ESTs, Moderately similar to HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 [H.sapiens]
15	1.6e-106:527:97
	Hs.86362:AA205485
	R-NT2RP2005247
	MHC class II transactivator
20	7.9e-35:465:69
	Hs.3076:U18259
	R-NT2RP2005378
	ESTs
25	3.4e-110:566:94
	Hs.23060:N64748
	R-NT2RP2005391
	ESTs
30	5.5e-82:463:92
	Hs.118793:AA192438
	R-NT2RP2005425
	Homo sapiens mRNA for KIAA0803 protein, partial cds
35	2.6e-101:526:94
	Hs.58103:AB018346
	R-NT2RP2005463
	ESTs, Weakly similar to weakly similar to S. cervisiae PTM1 precursor [C.elegans]
40	7.6e-111:554:97
	Hs.16492:N95400
	R-NT2RP2005514
	ESTs
45	1.8e-97:490:95
	Hs.109677:AA447864
	R-NT2RP2005535
	EST
50	5.1e-40:399:73
	Hs.127142:AA937570
	R-NT2RP2005541
	ESTs
55	5.2e-114:573:96
	Hs.70823:AI378619
	R-NT2RP2005597

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- ESTs, Weakly similar to rotated abdomen protein [D.melanogaster]
3.7e-109:543:96
Hs.99654:AA670164
- 5 R-nnnnnnnnnnnnn
ESTs
1.1 e-100:501:97
Hs.112011:AA987961
- 10 R-NT2RP2005666
ESTs
2.7e-106:560:94
Hs.42814:AA205754
- 15 R-NT2RP2005774
Homo sapiens apoptosis-related mRNA, 3'UTR, partial sequence
7.0e-96:440:96
Hs.139345:AF035364
- 20 R-NT2RP2005878
ESTs
2.8e-89:479:93
Hs.142305:R42591
- 25 R-NT2RP2005883
ESTs
1.0e-85:431:96
Hs.6909:AA928115
- 30 R-NT2RP2005887
ESTs
5.5e-109:566:94
Hs.12305:AA166889
- 35 R-nnnnnnnnnnnnn
Paired box homeotic gene 6 (aniridia, keratitis)
1.6e-116:578:96
Hs.89506:M93650
- 40 R-NT2RP2005994
EST
0.0061:129:68
Hs.160756:AI310589
- 45 R-NT2RP2006004
ESTs, Weakly similar to KIAA0405 [H.sapiens]
4.7e-45:303:86
Hs.14146:W92235
- 50 R-NT2RP2006042
EST
0.64:84:71
Hs.133275:AI053487
- 55 R-NT2RP2006092
ESTs, Weakly similar to HYPOTHETICAL PROTEIN KIAA0168 [H.sapiens]
1.1e-75:384:95
Hs.32822:AI194045

R-NT2RP2006099
 ESTs
 6.9e-35:224:82
 Hs.139446:AA461080
 5
 R-NT2RP2006134
 EST
 1.3e-95:445:100
 Hs.162033:AA514590
 10
 R-NT2RP2006269
 Human mRNA for KIAA0315 gene, partial cds
 0.96:343:60
 Hs.3989:AB002313
 15
 R-NT2RP2006512
 Homo sapiens clone 23904 mRNA sequence
 1.5e-107:531:96
 Hs.67364:AF052129
 20
 R-NT2RP3000011
 ESTs
 7.3e-92:508:91
 Hs.112041:W26001
 25
 R-NT2RP3000022
 EST
 0.78:175:63
 Hs.135650:AA902912
 30
 R-NT2RP3000059
 ESTs
 6.2e-99:475:98
 Hs.123136:AA631067
 35
 R-NT2RP3000063
 ESTs
 9.7e-105:554:94
 Hs.7542:AA121663
 40
 R-nnnnnnnnnnnnn
 Human mRNA for KIAA0314 gene, partial cds
 5.0e-17:307:65
 Hs.155045:AB002312
 45
 R-NT2RP3000148
 ESTs
 6.4e-101:527:94
 Hs.58461:W80378
 50
 R-NT2RP3000169
 Homo sapiens MRS1 mRNA, complete cds
 1.4e-111:551:96
 Hs.30985:AF093239
 55
 R-NT2RP3000171
 EST
 0.45:205:57

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Hs.147759:AI220726

R-NT2RP3000172

ESTs

5 2.0e-89:494:93

Hs.6262:T89093

R-NT2RP3000201

Human mRNA for KIAA0355 gene, complete cds

10 1.1e-40:305:83

Hs.153014:AB002353

R-NT2RP3000232

ESTs, Weakly similar to kruppel-related zinc finger protein [H.sapiens]

15 5.7e-65:386:90

Hs.4841:AI279875

R-NT2RP3000304

Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds

20 1.1e-109:541:97

Hs.23672:AF074264

R-NT2RP3000378

EST

25 2.0e-05:112:74

Hs.137268:T39311

R-NT2RP3000436

EST

30 1.2e-08:347:62

Hs.158830:AI377454

R-NT2RP3000444

ESTs

35 3.3e-70:314:99

Hs.57973:AI263207

R-NT2RP3000460

EST

40 1.9e-50:294:92

Hs.7260:T23737

R-NT2RP3000481

PROBABLE G PROTEIN-COUPLED RECEPTOR GPR6

45 1.0:183:59

Hs.46332:U18549

R-NT2RP3000616

ESTs

50 3.0e-71:309:93

Hs.41296:N71923

R-NT2RP3000645

ESTs

55 1.5e-101:550:92

Hs.21910:AA020743

R-NT2RP3000652

- ESTs
6.6e-88:411:100
Hs.43134:AA766138
- 5 R-NT2RP3000676
Homo sapiens mRNA for KIAA0446 protein, complete cds
1.0e-104:542:94
Hs.158286:AB007915
- 10 R-NT2RP3000677
ESTs
0.33:307:59
Hs.133022:AI374739
- 15 R-NT2RP3000721
ESTs
1.6e-75:390:90
Hs.83575:N28730
- 20 R-NT2RP3000789
ESTs
1.5e-71:340:99
Hs.37776:H93038
- 25 R-NT2RP3000818
ESTs
1.9e-52:330:88
H.s.111052:H80504
- 30 R-NT2RP3000820
EST
9.1e-05:82:74
Hs.124352:AA830406
- 35 R-NT2RP3000838
Homo sapiens mRNA for KIAA0638 protein, partial cds
1.5e-100:522:94
Hs.77864:AB014538
- 40 R-NT2RP3000871
ESTs
3.9e-76:424:91
Hs.121642:AA772262
- 45 R-NT2RP3000907
ESTs, Weakly similar to PROBABLE CATION-TRANSPORTING ATPASE YEL031W [Saccharomyces cerevisiae]
4.5e-95:493:94
Hs.9275:AA973284
- 50 R-NT2RP3000921
ESTs
4.1e-52:283:94
Hs.49714:AA442453
- 55 R-NT2RP3001012
Homo sapiens mRNA for CMP-sialic acid transporter, complete cds
0.60:250:61
Hs.82921:D87969

5 R-NT2RP3001044
ESTs
3.5e-106:547:95
Hs.12305:AA166889

10 R-NT2RP3001061
ESTs
1.3e-96:453:99
Hs.4916:AI149707

15 R-NT2RP3001159
ESTs, Weakly similar to T13F2.1 [C.elegans]
3.8e-47:302:90
Hs.6281:AA523081

20 R-NT2RP3001170
Homo sapiens mRNA for KIAA0784 protein, partial cds
2.8e-118:561:98
Hs.3657:AB018327

25 R-NT2RP3001195
ESTs
1.5e-40:461:72
Hs.152438:AI334078

30 R-NT2RP3001240
EST
1.9e-50:294:92
Hs.7260:T23737

35 R-NT2RP3001271
ESTs
1.1e-77:432:92
Hs.12211:AA908631

40 R-NT2RP3001322
ESTs
0.25:331:60
Hs.44330:N32264

45 R-NT2RP3001542
EST
0.0032:432:58
Hs.148107:AA693476

50 R-NT2RP3001560
EST
3.5e-50:281:93
Hs.101727:H16171

55 R-NT2RP3001592
ESTs
3.2e-65:344:93
Hs.28964:AA715101

R-NT2RP3001685
EST
3.0e-37:165:81

- Hs.160895:AI365871
- R-NT2RP3001738
ESTs, Weakly similar to T13F2.1 [C.elegans]
5 3.8e-47:302:90
Hs.6281:AA523081
- R-NT2RP3001754
EST
10 0.00043:104:69
Hs.148331:AA911426
- R-NT2RP3001858
ESTs
15 7.6e-93:502:93
Hs.153524:AA533582
- R-NT2RP3001976
ESTs
20 5.0e-104:516:96
Hs.35461:AA777644
- R-NT2RP3002015
- 25 R-NT2RP3002160
ESTs
1.4e-34:178:99
Hs.130783:AI263114
- 30 R-NT2RP3002281
Homo sapiens mRNA for KIAA0765 protein, partial cds
3.5e-83:446:93
Hs.62318:AB018308
- 35 R-NT2RP3002286
ESTs
2.1e-103:513:97
Hs.58570:AA521423
- 40 R-NT2RP3002311
ESTs
1.4e-108:538:96
Hs.3741:AI057614
- 45 R-NT2RP3002324
ESTs
3.7e-102:483:99
Hs.99668:AA829521
- 50 R-NT2RP3002342
ESTs, Weakly similar to transporter protein [H.sapiens]
2.0e-60:339:95
Hs.18272:N78499
- 55 R-NT2RP3002353
ESTs
6.8e-98:484:97
Hs.9732:AA527784

NNNNNNNNNNNNNNNN

Homo sapiens mRNA for KIAA0788 protein, partial cds

2.7e-29:214:85

Hs.2397:Z70200

5

NNNNNNNNNNNNNNNN

ESTs

3.0e-72:389:94

Hs.32246:AA464020

10

R-NT2RP3002448

ESTs, Weakly similar to Y48E1B.t [C.elegans]

1.0e-19:131:75

Hs.8715:H58021

15

R-NT2RP3002571

ESTs

1.1e-78:407:95

Hs.27356:AA740928

20

R-NT2RP3002664

ESTs

1.2e-56:341:90

Hs.23308:AA115020

25

R-NT2RP3002721

EST

2.8e-41:302:82

Hs.124936:AA825548

30

R-NT2RP3002737

EST

1.7e-51:267:97

Hs.161348:AI422470

35

R-NT2RP3002738

ESTs, Weakly similar to enhancer of filamentation 1 [H.sapiens]

1.7e-106:530:96

Hs.4894:AI191323

40

R-NT2RP3002790

R-NT2RP3002836

ESTs

4.6e-49:282:92

Hs.107979:AA146994

45

R-NT2RP3002887

ESTs

6.3e-98:516:94

Hs.11900:AA535065

50

R-NT2RP3002900

ESTs

2.0e-29:155:99

Hs.153329:AA112325

55

R-NT2RP3002958

- Homo sapiens clone 23851 mRNA sequence
6.6e-119:575:98
Hs.10065:AF035313
- 5 R-NT2RP3002983
ESTs
1.1e-61:374:90
Hs.17834:AA128246
- 10 R-NT2RP3003000
Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds
4.1e-65:358:94
Hs.122359:AF051946
- 15 R-NT2RP3003076
ESTs
2.6e-95:507:93
Hs.21910:AA020743
- 20 R-NT2RP3003354
ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H.sapiens]
2.1e-78:385:96
Hs.92177:AI207792
- 25 R-NT2RP3003448
ESTs
6.7e-105:521:96
Hs.106833:AA470128
- 30 R-NT2RP3003469
ESTs
1.1e-91:461:96
Hs.75425:AA149434
- 35 R-NT2RP3003473

R-NT2RP3003527
Homo sapiens mRNA for protein kinase Dyrk1B
1.6e-92:445:97
Hs.130988:Y17999
- 40 R-NT2RP3003532
ESTs
0.022:193:63
Hs.122593:Z99400
- 45 R-ntnnnnnnnnnnnn
EST
0.036:279:59
Hs.158745:AI375513
- 50 R-NT2RP3003559
ESTs
9.8e-106:513:97
Hs.44970:AI061464
- 55 R-NT2RP3003614
Homo sapiens mRNA, chromosome 1 specific transcript KIAA0510

	0.00016:113:69
	Hs.92660:AB007979
5	R-NT2RP3003729
	ESTs
	1.2e-43:289:86
	Hs.106401:R50967
10	R-NT2RP3003849
	ESTs
	5.4e-91:435:98
	Hs.144840:AI221746
15	R-NT2RP3003874
	ESTs
	0.21:323:59
	Hs.42919:AA805764
20	R-NT2RP3003963
	ESTs
	1.7e-90:438:97
	Hs.105894:AA564110
25	R-NT2RP3004000
	ESTs
	2.9e-101:559:91
	Hs.21910:AA020743
30	R-NT2RP3004025
	ESTs
	2.3e-108:517:98
	Hs.15356:AA911109
35	R-NT2RP3004075
	ESTs
	7.4e-84:453:93
	Hs.22412:AA523036
40	R-NT2RP3004083
	ESTs, Weakly similar to R06B9.b [C.elegans]
	4.2e-84:474:91
	Hs.30432:W28988
45	R-NT2RP3004090
	ESTs
	1.0:207:61
	Hs.92832:AA631027
50	R-NT2RP3004119
	EST
	1.8e-50:248:99
	Hs.162023:AA506128
55	R-NT2RP3004130
	ESTs
	1.1e-103:520:96
	Hs.10491:W28968

5 R-NT2RP3004133
ESTs
4.7e-104:545:93
Hs.15727:H98190

10 R-NT2RP3004202
ESTs
1.1e-98:471:98
Hs.61884:AI335985

15 R-NT2RP3004294
ESTs, Weakly similar to R06B9.b [C.elegans]
2.4e-96:500:94
Hs.30432:W28988

20 R-NT2RP3004309
ESTs, Weakly similar to T13F2.1 [C.elegans]
3.5e-48:308:90
Hs.6281:AA523081

25 R-NT2RP3004321
ESTs
2.6e-99:494:97
Hs.19306:N53491

30 R-NT2RP3004345
ESTs
5.4e-95:444:99
Hs.107149:AI379497

35 R-NT2RP3004355
ESTs
3.9e-99:490:97
Hs.43410:N23651

40 R-NT2RP3004374
ESTs
1.2e-90:462:95
Hs.75425:AA149434

45 R-NT2RP3004406
ESTs
1.9e-100:502:96
Hs.24936:AA479402

50 R-NT2RP3004481
ESTs
1.6e-53:370:87
Hs.11953:AA194120

55 R-NT2RP3004552
ESTs, Weakly similar to gene SEZ-6 [M.musculus]
7.8e-92:488:93
Hs.6314:AA522619

R-NT2RP3004625
Homo sapiens I-1 receptor candidate protein mRNA, complete cds
2.6e-50:352:84

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Hs.26285:AF082516

R-NT2RP3004640
ESTs
5 1.1e-105:551:94
Hs.83348:AA527170

R-NT2RP3004647
Homo sapiens mRNA for KIAA0446 protein, complete cds
10 4.9e-111:555:96
Hs.158286:AB007915

R-NT2RP4000108
ESTs
15 2.9e-94:479:96
Hs.6625:AA115182

R-NT2RP4000634
ESTs
20 3.0e-120:572:98
Hs.28827:AI125541

R-NT2RP4000962
ESTs, Weakly similar to SPORULATION-SPECIFIC PROTEIN 1 [Saccharomyces cerevisiae]
25 6.0e-17:98:98
Hs.4789:AI418298

R-NT2RP4001001
ESTs
30 3.1e-117:567:97
Hs.4931:AA523860

R-NT2RP4001009
Homo sapiens mRNA for Hs Ste24p, complete cds
35 1.6e-83:404:98
Hs.25846:AB016068

R-NT2RP4001467
5' nucleotidase (CD73)
40 5.9e-113:545:97
Hs.153952:X55740

R-NT2RP4001877
ESTs, Highly similar to GONADOTROPIN-RELEASING HORMONE RECEPTOR [Rattus norvegicus]
45 2.2e-67:375:93
Hs.16389:AA206356

R-NT2RP4001879

R-NT2RP4002187
EST
50 0.010:117:70
Hs.160416:AI394161

R-NT2RP4002451
EST
55 1.3e-62:386:87
Hs.57082:H25761

- 5 R-NT2RP4002715
ESTs
6.9e-111:552:96
Hs.12305:AA166889
- 10 R-NT2RP4002750
ESTs, Moderately similar to HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 [H.sapiens]
7.0e-109:532:97
Hs.86362:AA205485
- 15 R-OVARC1000003
ESTs
1.3e-74:391:95
Hs.105039:AA477819
- 20 R-OVARC1000090
Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds
9.9e-44:471:75
Hs.129735:AF010144
- 25 R-OVARC1000105
60S RIBOSOMAL PROTEIN L38
8.8e-14:83:100
Hs.2017:Z26876
- 30 R-OVARC1000137
ESTs
3.0e-84:387:95
Hs.22028:AA167715
- 35 R-OVARC1000208
Human mRNA for KIAA0392 gene, partial cds
2.8e-51:313:89
Hs.40100:AB002390
- 40 R-OVARC1000255
Spleen tyrosine kinase
2.8e-106:510:98
Hs.74101:L28824
- 45 R-OVARC1000275
ESTs, Highly similar to PROBABLE PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE FAB [Saccharomyces cerevisiae]
6.9e-105:556:94
Hs.5748:AA608559
- 50 R-OVARC1000298
ESTs, Weakly similar to T03G11.6 gene product [C.elegans]
2.4e-56:338:90
Hs.108354:W19984
- 55 R-OVARC1000307
ESTs
2.4e-101:563:93
Hs.24479:N25972
- R-OVARC1000313
Homo sapiens mRNA for KIAA0573 protein, partial cds

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- 5.0e-98:534:93
Hs.154023:AB011145
- 5 R-OVARC1000331
Homo sapiens chromosome 9, P1 clone 11659
1.0e-55:281:97
Hs.3439:AC004472
- 10 R-OVARC1000410
Homo sapiens clone 23767 and 23782 mRNA sequences
3.3e-90:462:94
Hs.8025:AF007150
- 15 R-OVARC1000439
ESTs, Highly similar to HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III
[Caenorhabditis elegans]
1.6e-99:510:95
Hs.7471:AI143226
- 20 R-OVARC1000467
- R-OVARC1000529
ESTs
5.7e-93:461:96
- 25 Hs.21396:AA114834
- R-OVARC1000553
ESTs
4.3e-51:351:87
- 30 Hs.42979:W31096
- R-OVARC1000775
- 35 R-OVARC1000811
ESTs
1.3e-82:441:95
Hs.73452:AA581386
- 40 R-OVARC1000853
ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
3.1e-95:492:95
Hs.6853:AA401703
- 45 R-OVARC1000873
ESTs
2.4e-46:281:91
Hs.43857:R91358
- 50 R-OVARC1000916
H.sapiens PISSLRE mRNA
1.9e-112:588:94
Hs.77313:X78342
- 55 R-OVARC1000956
Homo sapiens mRNA for MDC3, complete cds
0.18:259:62
Hs.7164:AB009672

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R-OVARC1000995
 EST
 6.6e-43:343:81
 Hs.149580:AI281881
 5

R-OVARC1001030
 ESTs, Weakly similar to neuroendocrine-specific protein C [H.sapiens]
 1.5e-21:116:100
 Hs.65450:AA055913
 10

R-OVARC1001049
 ESTs
 1.2e-70:369:95
 Hs.42949:N21131
 15

R-OVARC1001086
 Homo sapiens cyclin T2a mRNA, complete cds
 1.3e-106:569:94
 Hs.155478:AF048731
 20

R-OVARC1001132
 INITIATION FACTOR IF-2, MITOCHONDRIAL PRECURSOR
 0.16:170:64
 Hs.149894:L34600
 25

R-OVARC1001163
 ESTs
 1.9e-39:219:94
 Hs.126067:AI344351
 30

R-OVARC1001222
 ESTs
 0.62:177:63
 Hs.141162:H66213
 35

R-OVARC1001260
 ESTs
 2.1e-79:425:94
 Hs.105039:AA477819
 40

R-OVARC1001336
 ESTs
 9.2e-75:439:91
 Hs.105039:AA477819
 45

R-OVARC1001338
 ESTs
 2.3e-19:139:92
 Hs.7978:W05059
 50

R-OVARC1001569
 ESTs
 2.4e-83:412:97
 Hs.21396:AA114834
 55

R-OVARC1001570
 ESTs
 2.6e-49:280:94

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Hs.3854:R12478

R-OVARC1001596
EST
5 8.2e-15:93:97
Hs.136918:AA811543

R-OVARC1001607
ESTs
10 0.019:413:56
Hs.24684:AA587245

R-OVARC1001725
ESTs
15 1.4e-96:504:95
Hs.23754:N29716

R-OVARC1001727

20 R-OVARC1001807
Hormone receptor (growth factor-inducible nuclear protein N10)
8.5e-78:425:94
Hs.1119:D49728

25 R-OVARC1001833
ESTs
1.0e-63:325:96
Hs.126912:AA469087

30 R-OVARC1001991
ESTs
1.3e-92:467:95
Hs.26506:AI348000

35 R-OVARC1002058
ESTs
2.5e-89:512:91
Hs.58093:W63576

40 R-OVARC1002178
ESTs
3.3e-99:487:96
Hs.136527:AI419398

45 R-PLACE1000033
ESTs
0.012:202:59
Hs.157400:AI370528

50 R-PLACE1000231
ESTs
2.9e-56:285:96
Hs.36688:AA603479

55 R-PLACE1000258
EST
3.4e-50:353:83
Hs.146794:AI149478

- 5
R-PLACE1000442
ESTs, Moderately similar to ZINC FINGER PROTEIN ZFP-36 [Homo sapiens]
5.5e-91:437:98
Hs.14831:AI261191
- 10
R-PLACE1000560
ESTs
3.7e-60:317:94
Hs.65713:AI269328
- 15
R-PLACE1000740
ESTs
4.2e-67:362:94
Hs.163434:T79849
- 20
R-PLACE1000912
ESTs
3.4e-57:329:92
Hs.121907:R66773
- 25
R-PLACE1000914
ESTs
2.6e-71:419:89
Hs.90809:AA010979
- 30
R-PLACE1000927
ESTs, Weakly similar to N-methyl-D-aspartate receptor-associated protein [D.melanogaster]
7.8e-111:545:97
Hs.8661:AI189791
- 35
R-PLACE1000986
ESTs
1.5e-91:431:99
Hs.42458:AA452296
- 40
R-PLACE1001016
ESTs
3.4e-45:231:97
Hs.121013:AA324765
- 45
R-PLACE1001100
Homo sapiens nephrin (NPHS1) mRNA, complete cds
3.5e-43:321:83
Hs.128834:AF035835
- 50
R-PLACE1001114
Human clone 23732 mRNA, partial cds
1.6e-42:305:83
Hs.81281:U79258
- 55
R-PLACE1001123
ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD [Saccharomyces cerevisiae]
1.2e-51:310:90
Hs.7773:AA127629
- R-PLACE1001183
Human mRNA for KIAA0308 gene, partial cds

0.88:182:65
Hs.10351:AB002306

5 R-PLACE1001229
ESTs
5.2e-90:471:95
Hs.18271:N92774

10 R-PLACE1001231

R-PLACE1001340
Homo sapiens mRNA for KIAA0719 protein, complete cds
6.6e-53:265:98
Hs.21198:AB018262

15 R-PLACE1001401
ESTs
1.9e-72:362:96
Hs.20161:AA056410

20 R-PLACE1001407
ESTs
2.1e-36:249:85
Hs.23579:W38893

25 R-PLACE1001464
5' nucleotidase (CD73)
1.0e-91:457:96
Hs.153952:X55740

30 R-PLACE1001500
ESTs, Weakly similar to DNA helicase Q1 [H.sapiens]
2.0e-19:150:87
Hs.154199:AA155882

35 R-PLACE1001516
EST
1.9e-11:109:82
Hs.137486:AA425225

40 R-PLACE1001536
Human BRCA2 region, mRNA sequence CG016
0.28:146:63
Hs.112434:U50529

45 R-PLACE1001564
ESTs
6.3e-14:109:88
Hs.26519:AA442703

50 R-PLACE1001655
Homo sapiens Shab-related delayed-rectifier K⁺ channel alpha subunit (KCNS3) mRNA, complete cds
1.2e-118:578:97
Hs.47584:AF043472

55 R-PLACE1001788
ESTs
8.4e-38:205:95

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Hs.23800:AA524095

R-PLACE1001795

ESTs, Weakly similar to HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-MRPL8 INTERGENIC REGION PRE-CURSOR [S.cerevisiae]

2.5e-77:392:96

Hs.7745:H92988

R-PLACE1001836

ESTs

1.5e-49:296:90

Hs.17691:H60366

R-PLACE1001918

ESTs, Weakly similar to multispinning membrane protein [H.sapiens]

2.0e-42:304:85

Hs.110439:N93209

R-PLACE1001949

R-PLACE1002080

Small inducible cytokine A5 (RANTES)

8.5e-41:296:82

Hs. 155464:AF088219

R-PLACE1002095

ESTs

8.5e-25:227:81

Hs.110488:AA034235

R-PLACE1002153

Homo sapiens TACC2 protein (TACC2) mRNA, partial cds

1.5e-101:514:95

Hs.90415:AF095791

R-PLACE1002329

ESTs

8.7e-48:257:94

Hs.126062:AA411593

R-PLACE1002355

ESTs

7.7e-71:362:95

Hs.120866:AI076780

R-PLACE1002374

Cathepsin L

8.4e-103:501:97

Hs.78056:X12451

R-PLACE1002518

ESTs

6.9e-97:471:97

Hs.104893:AA576941

R-PLACE1002547

Homo sapiens mRNA for KIAA0719 protein, complete cds

6.5e-55:276:97

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Hs.21198:AB018262

R-PLACE1002726

Human DNA-binding protein ABP/ZF mRNA, complete cds

3.8e-39:212:94

Hs.86185:U82613

R-PLACE1002905

Homo sapiens mRNA for KIAA0563 protein, complete cds

2.9e-41:330:81

Hs.15731:AB011135

R-PLACE1002911

R-PLACE1002967

ESTs

1.0e-43:384:77

Hs.132722:AA618531

R-PLACE1003135

ESTs

8.2e-94:462:97

Hs.23643:AI299952

R-PLACE1003163

Homo sapiens DBI-related protein mRNA, complete cds

3.5e-110:541:96

Hs.15250:AF069301

R-PLACE1003407

Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds

5.5e-49:287:91

Hs.30213:AF068227

R-PLACE1003428

ESTs, Moderately similar to BIOTINIDASE PRECURSOR [Homo sapiens]

6.8e-83:406:97

Hs.17586:AA461448

R-PLACE1003438

ESTs

2.9e-83:463:92

Hs.11067:H30385

R-PLACE1003460

ESTs

7.0e-27:187:87

Hs.18763:H56292

R-nnnnnnnnnnnnn

ESTs

1.7e-52:265:97

Hs.114049:AI091839

R-PLACE1003573

Human mRNA for KIAA0160 gene, partial cds

0.13:102:69

Hs.79880:D63881

5 R-PLACE1003598
ESTs
8.0e-39:210:95
Hs.26286:AA040823

10 R-PLACE1003644
EST
0.47:84:73
Hs.105856:AA551478

15 R-PLACE1003737
ESTs
1.1e-77:366:100
Hs.62699:AA707766

20 R-PLACE1003772
Human mRNA for KIAA0355 gene, complete cds
6.1e-27:551:65
Hs.153014:AB002353

25 R-PLACE1003839
ESTs
0.019:244:59
Hs.137825:AA778400

30 R-PLACE1003845
EST
5.3e-79:416:93
Hs.150153:AI300555

35 R-PLACE1003852
Homo sapiens mRNA for KIAA0758 protein, partial cds
2.2e-87:439:96
Hs.22039:AB018301

40 R-PLACE1004028
Sialyltransferase 4A (beta-galactosidase alpha-2,3-sialyltransferase)
0.73:128:71
Hs.60617:L13972

45 R-PLACE1004078
ESTs
1.7e-69:353:96
Hs.142075:AA654529

50 R-PLACE1004166
ESTs
1.7e-64:362:92
Hs.10177:AA191619

55 R-PLACE1004199
ESTs
1.3e-55:279:97

- Hs.147585:AI217699
- R-PLACE1004279
ESTs
5 3.7e-68:373:93
Hs.145531:H87181
- R-PLACE1004282
- 10 R-PLACE1004305
Homo sapiens mRNA for KIAA0740 protein, complete cds
6.4e-79:377:99
Hs.15099:AB018283
- 15 R-PLACE1004441
ESTs
1.8e-46:244:95
Hs.107082:R63714
- 20 R-PLACE1004450
- R-PLACE1004482
ESTs
1.2e-92:491:93
25 Hs.17840:AI269915
- R-PLACE1004492
ESTs
6.1e-54:278:95
30 Hs.55862:A1341676
- R-PLACE1004519
ESTs
3.1e-25:133:100
35 Hs.47378:AI193598
- R-PLACE1004520
Pregnancy-specific beta-1 glycoprotein 4
2.8e-66:390:89
40 Hs.108936:X17097
- R-PLACE1004630
ESTs
7.3e-58:338:92
45 Hs.155506:AI281549
- R-PLACE1004637
ESTs
1.1e-37:309:82
50 Hs.20102:AA150165
- R-PLACE1004648
ESTs
2.3e-67:340:96
55 Hs.69321:AA633240
- R-PLACE1004816
Homo sapiens mRNA for Hakata antigen, complete cds

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- 1.8e-104:586:90
Hs.9225:D88587
- 5 R-PLACE1004887
ESTs, Weakly similar to GOLIATH PROTEIN [D.melanogaster]
2.6e-30:222:86
Hs.18557:AA203416
- 10 R-PLACE1005003
ESTs
0.99:123:68
Hs.146244:AI276718
- 15 R-PLACE1005005
Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds
6.8e-58:299:95
Hs.151614:AF032456
- 20 R-PLACE1005031
ESTs
4.7e-57:325:92
Hs.31196:H13265
- 25 R-PLACE1005239
Homo sapiens mRNA for HIRIP3 protein, clone pH4-17
1.4e-86:450:93
Hs.26484:AJ223351
- 30 R-PLACE1005250
ESTs, Moderately similar to maternal transcript Maid [M.musculus]
1.7e-106:521:97
Hs.36794:AI038407
- 35 R-PLACE1005383
Homo sapiens UP50 mRNA, complete cds
6.3e-79:471:88
Hs.11494:AF093118
- 40 R-PLACE1005410
EST
2.3e-49:296:90
Hs.7260:T23737
- 45 R-PLACE1005426
Pregnancy-specific beta-1 glycoprotein 4
8.0e-109:576:93
Hs.108936:X17097
- 50 R-PLACE1005519
ESTs
5.4e-108:569:93
Hs.23643:AI299952
- 55 R-PLACE1005539
ESTs, Weakly similar to p20 protein [R.norvegicus]
4.5e-05:107:77
Hs.56874:W61026

- 5 R-PLACE1005544
ESTs
4.2e-57:280:98
Hs.155391:AA451633
- 10 R-PLACE1005569
ESTs
2.7e-90:470:94
Hs.8904:AI129815
- 15 R-PLACE1005601

R-PLACE1005660
ESTs, Highly similar to HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III
[Caenorhabditis elegans]
1.4e-91:483:93
Hs.7471:AI143226
- 20 R-PLACE1005669
ESTs
1.7e-84:438:95
Hs.18271:N92774
- 25 R-PLACE1005682
ESTs
6.3e-80:482:88
Hs.128679:AI160081
- 30 R-PLACE1005725
ESTs
1.5e-98:519:93
Hs.11360:AI147467
- 35 R-PLACE1005736
ESTs
3.1e-110:561:95
Hs.24111:AI346026
- 40 R-PLACE1005745
ESTs
2.4e-96:473:97
Hs.126935:AA603217
- 45 R-PLACE1005768
Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2
4.0e-46:387:77
Hs.1361:M55053
- 50 R-PLACE1005815
Homo sapiens PYRIN (MEFV) mRNA, complete cds
7.1e-56:324:79
Hs.113283:AF018080
- 55 R-PLACE1005878
ESTs
3.1e-75:388:94
Hs.153483:AA569128

5
R-PLACE1005927
ESTs
4.3e-64:403:87
Hs.126899:N50907

10
R-PLACE1006071
ESTs
5.3e-96:510:93
Hs.24398:AI262946

15
R-PLACE1006073
Homo sapiens mRNA for glucuronyltransferase I, complete cds
3.0e-97:504:93
Hs.26492:AB009598

20
R-PLACE1006079
ESTs
3.1e-79:453:90
Hs.134194:AI142137

25
R-PLACE1006093
ESTs
1.3e-78:378:98
Hs.129327:AI201040

30
R-PLACE1006219
EST
1.6e-75:412:92
Hs.150153:AI300555

35
R-PLACE1006277
ESTs
2.8e-92:493:93
Hs.8904:AI129815

40
R-PLACE1006290
ESTs
2.8e-92:433:99
Hs.23445:AA489015

45
R-PLACE1006443
ESTs
2.5e-73:419:91
Hs.90809:AA010979

50
R-PLACE1006515
Homo sapiens mRNA for KIAA0576 protein, partial cds
6.9e-78:413:94
Hs.14687:AB011148

55
R-PLACE1006716
ESTs
4.8e-44:262:88
Hs.8503:AI393886

R-PLACE1006786

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- ESTs
6.3e-89:431:98
Hs.42458:AA452296
- 5 R-PLACE1006809
ESTs
1.6e-68:377:92
Hs.8956:AI146421
- 10 R-PLACE1006959
EST
0.00065:211:63
Hs.136605:AA665784
- 15 R-PLACE1007028
ESTs
7.4e-92:475:94
Hs.110222:AA532444
- 20 R-PLACE1007040
ESTs
5.1e-103:509:97
Hs.71190:AA524036
- 25 R-PLACE1007077
ESTs
1.0e-98:529:93
Hs.24398:AI262946
- 30 R-PLACE1007081
Human growth factor independence-1 (Gfi-1) mRNA, complete cds
0.57:238:61
Hs.73172:U67369
- 35 R-PLACE1007096
ESTs
1.2e-88:466:94
Hs.8268:N70144
- 40 R-PLACE1007296
EST
4.3e-53:338:86
Hs.147274:AI206582
- 45 R-PLACE1007591
EST
4.6e-76:384:97
Hs.94445:N90719
- 50 R-PLACE1007626
Homo sapiens unknown mRNA, complete cds
5.0e-30:179:91
Hs.11441:AF047439
- 55 R-PLACE1007702
ESTs
1.0e-52:341:87
Hs.103382:AA026923

- 5 R-PLACE1007845
ESTs
2.2e-102:541:93
Hs.15727:H98190
- 10 R-PLACE1007881
ESTs
4.1e-75:398:93
Hs.55560:AI142804
- 15 R-PLACE1007971
ESTs
2.8e-43:304:85
Hs.82933:AA058963
- 20 R-PLACE1008282
ESTs, Highly similar to HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE [Oryc-
tolagus cuniculus]
2.2e-74:393:94
Hs.77613:AI367385
- 25 R-PLACE1008297
ESTs
6.5e-101:506:96
Hs.44274:AA523749
- 30 R-PLACE1008359
ESTs
1.8e-94:469:96
Hs.160551:AI281417
- 35 R-PLACE1008469
ESTs
7.0e-74:421:90
Hs.90809:AA010979
- 40 R-PLACE1008549
ESTs
2.0e-81:474:90
Hs.11713:T65960
- 45 R-PLACE1008657
ESTs
9.5e-89:512:89
Hs.142075:AA654529
- 50 R-PLACE1008716
Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds
5.6e-100:504:95
Hs.154844:U15128
- 55 R-PLACE1008744
ESTs, Highly similar to COMPLEMENT RECEPTOR TYPE 2 PRECURSOR [Homo sapiens]
2.3e-107:528:96
Hs.8963:AI379350
- R-PLACE1008984
ESTs

- 2.0e-76:464:89
Hs.40094:D12041
- 5 R-PLACE1008985
EST, Highly similar to SYNAPTOTAGMIN B [Discopyge ommata]
2.2e-59:343:90
Hs.161031:H72014
- 10 R-PLACE1009067
ESTs
7.7e-90:503:92
Hs.55067:AA037664
- 15 R-PLACE1009196
EST
0.011:243:60
Hs.149839:AI287601
- 20 R-PLACE1009279
Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds
5.4e-27:553:62
Hs.75111:D87258
- 25 R-PLACE1009527
Human DNA-binding protein ABP/ZF mRNA, complete cds
2.7e-92:497:91
Hs.86185:U82613
- 30 R-PLACE1009546
ESTs
5.9e-80:461:90
Hs.134292:AA603031
- 35 R-PLACE1009600
ESTs
5.5e-98:509:93
Hs.21015:AA428288
- 40 R-PLACE1009735
ESTs
1.1e-85:462:93
Hs.48563:AA526595
- 45 R-aaaaaaaaaaaa
ESTs
6.8e-82:499:87
Hs.43498:AA570507
- 50 R-PLACE1010011
ESTs, Moderately similar to synaptonemal complex protein [M.musculus]
2.7e-15:171:78
Hs.31655:AI075991
- 55 R-PLACE1010078
ESTs
1.2e-48:267:92
Hs.12101:AA677423

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- 5 R-PLACE1010081
Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds
3.0e-106:560:93
Hs.103755:AF027706
- 10 R-PLACE1010251
ESTs
0.00049:248:60
Hs.154164:AI246893
- 15 R-PLACE1010445
ESTs
1.5e-90:496:92
Hs.163999:AA778110
- 20 R-PLACE1010713
Interleukin 1 receptor antagonist
4.1e-07:307:59
Hs.81134:U65590
- 25 R-PLACE1010784
ESTs, Weakly similar to putative G-protein-coupled receptor [H.sapiens]
1.5e-21:206:78
Hs.29202:R71586
- 30 R-PLACE1010827
- R-PLACE 1010968
ESTs
2.6e-75:385:95
Hs.109884:AA766018
- 35 R-PLACE1011045
Homo sapiens E1-like protein mRNA, complete cds
5.3e-92:453:96
Hs.28190:AF094516
- 40 R-PLACE1011116
Homo sapiens embryonic lung protein (HUEL) mRNA, complete cds
1.5e-73:385:94
Hs.44053:AF006621
- R-PLACE1011236
- 45 R-PLACE1011364
ESTs
2.3e-47:289:89
Hs.6163:W26652
- 50 R-PLACE1011407
ESTs
1.1e-09:191:64
Hs.118620:T60326
- 55 R-PLACE1011516
ESTs, Weakly similar to HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION [S.cerevisiae]
6.3e-75:441:88

Hs.110978:AA843431

R-PLACE1011708
Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds
5 7.7e-93:521:91
Hs.148318:AF034611

R-PLACE1011824
ESTs
10 0.013:199:62
Hs.44343:AA532514

R-PLACE1011978
EST
15 4.0e-97:462:98
Hs.116391:AA644085

R-PLACE2000118
ESTs
20 1.2e-83:468:92
Hs.110578:AA115763

R-PLACE2000219
Homo sapiens KIAA0414 mRNA, partial cds
25 2.0e-44:344:81
Hs.127649:AB007874

R-PLACE3000181
Human protocadherin 42 mRNA, 3' end of cds for alternative splicing PC42-8
30 1.3e-82:441:94
Hs.115642:L11369

R-PLACE3000213
ESTs, Highly similar to COMPLEMENT RECEPTOR TYPE 2 PRECURSOR [Homo sapiens]
35 2.3e-114:557:97
Hs.8963:AI379350

R-PLACE4000354
ESTs, Highly similar to COMPLEMENT RECEPTOR TYPE 2 PRECURSOR [Homo sapiens]
40 3.4e-105:518:97
Hs.8963:AI379350

R-PLACE4000455
ESTs
45 9.0e-57:289:96
Hs.42458:AA452296

R-THYRO1000036
Collagen, type IX, alpha 3
50 1.3e-100:527:93
Hs.53563:L41162

R-THYRO1000061
ESTs
55 1.8e-87:460:94
Hs.124869:H98977

R-THYRO1000099

- ESTs
1.2e-34:193:94
Hs.149488:AI243816
- 5 R-THYRO1000196
Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds
3.7e-106:530:96
Hs.115418:AF016272
- 10 R-THYRO1000400
Human HU-K4 mRNA, complete cds
0.99:227:60
Hs.74573:U60644
- 15 R-THYRO1000580
Homo sapiens mRNA for KIAA0628 protein, complete cds
0.21:126:67
Hs.43133:AB014528
- 20 R-THYRO1000584
ESTs, Weakly similar to golgi alpha-mannosidase II [H.sapiens]
3.0e-106:529:96
Hs.12183:AA888145
- 25 R-THYRO1000678
EST
2.9e-62:304:99
Hs.48956:N64339
- 30 R-THYRO1000776
ESTs
1.3e-102:533:94
Hs.4866:AA582196
- 35 R-THYRO1000795
ESTs
3.3e-98:529:92
Hs.55263:AI344338
- 40 R-THYRO1000846
ESTs
1.6e-105:522:96
Hs.135106:AI335251
- 45 R-THYRO1000866
Homo sapiens SKB1Hs mRNA, complete cds
1.3e-43:251:92
Hs.12912:AF015913
- 50 R-THYRO1000956
ESTs, Highly similar to PROBABLE G PROTEIN-COUPLED RECEPTOR APJ [Homo sapiens]
5.2e-106:548:94
Hs.9305:W84893
- 55 R-THYRO1000964

R-THYRO1000999
ESTs

1.9e-18:150:84
Hs.111583:AA463590

5 R-THYRO1001063
ESTs
1.5e-95:464:97
Hs.142684:AA902402

10 R-THYRO1001071
ESTs
2.5e-104:496:98
Hs.6071:AA868544

15 R-THYRO1001102
R-THYRO1001113
ESTs, Weakly similar to FER-1 [C.elegans]
7.1e-90:446:97
Hs.8076:AA115644

20 R-THYRO1001128
ESTs
1.9e-16:270:68
Hs.140194:N35720

25 R-THYRO1001205
Small inducible cytokine A5 (RANTES)
1.9e-58:400:84
Hs.155464:AF088219

30 R-THYRO1001237
ESTs
1.5e-104:532:96
Hs.6603:AA772122

35 R-THYRO1001242
EST
1.7e-50:281:93
Hs.101727:H16171

40 R-THYRO1001266
Homo sapiens mRNA for KIAA0650 protein, partial cds
0.00037:403:60
Hs.8118:AB014550

45 R-THYRO1001327
ESTs
1.2e-96:530:93
Hs.28786:AA034412

50 R-THYRO1001456
ESTs, Weakly similar to Similar to phytoene desaturase [C.elegans]
3.3e-43:257:92
Hs.97031:AA773647

55 R-THYRO1001457
ESTs, Highly similar to MYOSIN LIGHT CHAIN KINASE [Dictyostelium discoideum]
4.8e-59:284:99

- Hs.9915:AI300083
- R-THYRO1001471
ESTs
5 1.1e-67:378:93
Hs.52113:R40587
- R-THYRO1001478
- 10 R-THYRO1001495
H.sapiens mRNA for Zinc-finger protein (ZNFpT17)
1.6e-63:434:84
Hs.32954:X65233
- 15 R-THYRO1001523
ESTs
5.8e-75:388:96
Hs.6527:R21517
- 20 R-THYRO1001529
ESTs
1.1e-25:184:87
Hs.18441:AA005104
- 25 R-THYRO1001593
ESTs
4.7e-34:182:98
Hs.8312:AA813022
- 30 R-THYRO1001608
ESTs
2.8e-107:547:95
Hs.23765:AA524283
- 35 R-THYRO1001641
Homo sapiens clone 24448 unknown mRNA, partial cds
1.1e-111:562:96
Hs.4973:AF070638
- 40 R-THYRO1001700
ESTs
1.3e-78:407:95
Hs.86987:N99896
- 45 R-THYRO1001702
ESTs
4.3e-98:566:92
Hs.119447:AA524436
- 50 R-THYRO1001725
ESTs
1.3e-84:424:96
Hs.38039:AI360128
- 55 R-THYRO1001770
ESTs
1.0e-62:325:97
Hs.20137:R08273

5 R-THYRO1001803
ESTs
6.8e-90:456:96
Hs.134438:R42585

10 R-Y79AA1000030
ESTs, Weakly similar to HYPOTHETICAL PROTEIN KIAA0168 [H.sapiens]
2.4e-98:515:94
Hs.32822:AI194045

15 R-Y79AA1000127
ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]
1.1e-57:307:95
Hs.83513:W05849

20 R-Y79AA1000207
EST
1.0e-97:411:96
Hs.141431:N21286

25 R-Y79AA1000226
ESTs, Highly similar to HYPOTHETICAL 52.8 KD PROTEIN T05E11.5 IN CHROMOSOME IV [Caenorhabditis
elegans]
7.2e-102:545:94
Hs.11221:AI192291

30 R-Y79AA1000270
Human mRNA for ORF, Xq terminal portion
3.3e-107:564:93
Hs.6551:D16469

35 R-Y79AA1000426
H.sapiens mRNA for activin beta-C chain
2.5e-10:217:66
Hs.83267:X82540

40 R-Y79AA1000521
Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds
0.73:257:59
Hs.113286:U77783

45 R-Y79AA1000750
ESTs
4.3e-75:391:95
Hs.157192:W84862

50 R-Y79AA1000776
ESTs
3.5e-56:303:95
Hs.118559:AA887084

55 R-Y79AA1000777
ESTs, Weakly similar to LIS-1 protein [H.sapiens]
9.5e-98:515:95
Hs.59461:W93217

R-Y79AA1000876
EST

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- 2.7e-23:173:84
Hs.135872:AI037885
- 5 R-Y79AA1000959
Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds
3.4e-80:453:92
Hs.53066:AF093420
- 10 R-Y79AA1000967
ESTs
7.3e-86:461:93
Hs.6262:T89093
- 15 R-Y79AA1001013
ESTs
1.4e-115:566:97
Hs.108408:N31922
- 20 R-Y79AA1001056
ESTs, Moderately similar to maternal transcript Maid [M.musculus]
8.7e-111:557:95
Hs.36794:AI038407
- 25 R-Y79AA1001062
ESTs
0.0021:365:59
Hs.106129:AA292171
- 30 R-Y79AA1001090
ESTs
5.0e-52:255:99
Hs.106214:AI123831
- 35 R-Y79AA1001212
Homo sapiens SL15 protein mRNA, complete cds
1.8e-83:407:97
Hs.6710:AF038961
- 40 R-Y79AA1001264
ESTs, Highly similar to DNAJ PROTEIN HOMOLOG 2 [Homo sapiens]
2.8e-111:552:96
Hs.62489:AI057091
- 45 R-Y79AA1001272
Zinc finger protein, X-linked
0.019:317:59
Hs.2074:X59739
- 50 R-Y79AA1001328
ESTs
3.6e-67:385:92
Hs.127792:AI421472
- 55 R-Y79AA1001426
ESTs
2.0e-13:92:93
Hs.105607:AA478379

5
R-Y79AA1001430
Homo sapiens mRNA for KIAA0469 protein, complete cds
2.0e-112:555:96
Hs.7764:AB007938

10
R-Y79AA1001523
EST
1.7e-07:120:73
Hs.130984:AI015430

15
R-Y79AA1001530
Homo sapiens RRM RNA binding protein Gry-rbp (GRY-RBP) mRNA, complete cds
0.030:169:63
Hs.155489:AF037448

20
R-Y79AA1001592
ESTs
5.0e-60:340:91
Hs.87019:AA760977

25
R-Y79AA1001727
ESTs
6.1e-101:547:93
Hs.7404:W29012

30
R-Y79AA1001787
ESTs
8.8e-84:449:95
Hs.128866:AA977749

35
R-Y79AA1001795
Homo sapiens mRNA for GalT4 protein
9.9e-110:541:97
Hs.21495:AL031228

40
R-Y79AA1001799
ESTs, Highly similar to MITOCHONDRIAL RNA SPLICING PROTEIN MSR4 [Saccharomyces cerevisiae]
1.6e-94:567:90
Hs.34401:AA447775

45
R-Y79AA1001803
ESTs, Highly similar to SECRETAGRANIN III PRECURSOR [Mus musculus]
1.2e-86:509:90
Hs.22215:AI371482

50
R-Y79AA1001863
ESTs
1.4e-23:268:73
Hs.131613:AI190576

55
R-Y79AA1002022
ESTs
8.9e-97:462:98
Hs.6140:D52151

R-nnnnnnnnnnnnn
R-nnnnnnnnnnnnn

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Homo sapiens DNA recombination and repair protein (MRE11B) mRNA, complete cds
0.00075:456:59
Hs.153855:AF022778

- 5 R-Y79AA1002213
Human mRNA for KIAA0392 gene, partial cds
6.2e-45:304:85
Hs.40100:AB002390
- 10 R-Y79AA1002334
ESTs
7.7e-91:495:92
Hs.90804:W28091
- 15 R-Y79AA1002373
Human kpni repeat mrna (cdna clone pcd-kpni-8), 3' end
5.2e-98:545:91
Hs.103948:K00627
- 20 R-Y79AA1002376
ESTs
2.0e-91:455:97
Hs.153375:AI287812
- 25 R-Y79AA1002378
ESTs, Highly similar to ZINC FINGER PROTEIN ZFP-35 [Mus musculus]
9.4e-15:131:83
Hs.20082:W89121
- 30 R-Y79AA1002381
ESTs, Highly similar to CELL DIVISION CONTROL PROTEIN 2 HOMOLOG [Plasmodium falciparum (isolate k1/thailand)]
1.5e-104:531:95
Hs.26322:AA156858

35 Homology search result 10

[0305] Data obtained by the homology search for full length nucleotide sequences and deduced amino acid sequences. In the result of the search shown below, both units, aa and bp, are used as length units for the sequences to be compared. Each data includes Clone name, Definition in matching data, P value, Length of sequence to be compared, Homology, and Accession number (No.) of matching data. These items are shown in this order, separated by a double-slash mark, //.

- 45 C-HEMBA1000006//Homo sapiens mRNA; cDNA DKFZp564G1762 (from clone DKFZp564G1762).//0//1230bp//92%//AB026894
C-nnnnnnnnnnnnn//GAMETOGENESIS EXPRESSED PROTEIN GEG-154.//2.30E-71//344aa//50%//P50636
C-HEMBA1000121//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.//4.80E-05//83aa//27%//P34679
- 50 C-HEMBA1000128//PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR-1).//3.20E-07//89aa//34%//P33154
C-HEMBA1000275
C-HEMBA1000300
C-HEMBA1000349//ATP-BINDING CASSETTE TRANSPORTER 1.//5.30E-65//352aa//39%//P41233
C-HEMBA1000443//Homo sapiens CGI-96 protein mRNA, complete cds.//4.70E-129//686bp//91%//AF151854
- 55 C-HEMBA1000590//Homo sapiens mRNA for matrilin-4, partial.//2.00E-273//1254bp//99%//AJ007581
C-HEMBA1000634//Homo sapiens T-cell activation protein (PGR1) gene, complete cds.//0//994bp//99%//AF116272
C-HEMBA1000713//Homo sapiens 10kD protein (BC10) mRNA, complete cds.//0//1254bp//99%//AF053470

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C-HEMBA1000745//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//2.00E-07//445aa//27%/P02454
 C-HEMBA1000907
 C-HEMBA1000940//GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44).//2.90E-39//362aa//31%/P41987
 5 C-HEMBA1000962
 C-HEMBA1001221//AGRIIN PRECURSOR.//2.50E-25//294aa//29%/P31696
 C-HEMBA1001228//Human germline oligomeric matrix protein (COMP) mRNA, complete cds.//7.80E-286//1105bp//94%/L32137
 C-HEMBA1001297
 10 C-HEMBA1001390//Mus musculus polymerase I-transcript release factor mRNA, complete cds.//2.50E-57//464bp//82%/AF036249
 C-HEMBA1001563
 C-HEMBA1001621//PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.//3.50E-123//259aa//89%/P35414
 C-nnnnnnnnnnnn//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.40E-85//293aa//50%/P51523
 15 C-HEMBA1001878//Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds.//0//1488bp//99%/AF090988
 C-HEMBA1002131//PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1//4.10E-10//140aa//30%/P24802
 20 C-HEMBA1002163//HYPOTHETICAL 40.7 KD PROTEIN IN DAK1-ORC1 INTERGENIC REGION.//9.40E-28//309aa//30%/Q04651
 C-HEMBA1002164
 C-HEMBA1002167//Rattus norvegicus neuroligin I mRNA, complete cds.//1.30E-305//1643bp//91%/U22952
 C-HEMBA1002178//PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HYDROXYLASE 1) (LH1).//3.70E-10//140aa//30%/P24802
 25 C-nnnnnnnnnnnn//Human glycyl-tRNA synthetase mRNA, complete cds.//0//2380bp//99%/U09587
 C-HEMBA1002195//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.80E-23//221aa//31%/Q00808
 C-HEMBA1002227//Homo sapiens mRNA for 80K-L protein, complete cds.//0//1324bp//98%/D10522
 C-HEMBA1002239
 30 C-HEMBA1002316
 C-HEMBA1002420
 C-HEMBA1002421//Human heparan sulfate proteoglycan (HSPG) core protein, 3' end.//0//2097bp//99%/J04621
 C-HEMBA1002524//Human MHC Class I region proline rich protein mRNA, complete cds.//0//1763bp//95%/U63336
 35 C-HEMBA1002551//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//9.80E-08//110aa//37%/P49695
 C-HEMBA1002767//Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds.//0//1497bp//99%/AF038660
 C-HEMBA1002992//UBIQUITIN-LIKE PROTEIN DSK2.//2.00E-21//216aa//35%/P48510
 40 C-HEMBA1003047//Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.//0//1768bp//99%/AF034611
 C-HEMBA1003072//Gallus gallus single-strand DNA-binding protein csdp mRNA, partial cds.//3.30E-93//927bp//73%/U68380
 C-HEMBA1003101//Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.//0//1854bp//99%/AF049891
 45 C-HEMBA1003230//Homo sapiens fibulin-5.//5.60E-308//1398bp//99%/AJ133490
 C-HEMBA1003294
 C-HEMBA1003315//Mus musculus mRNA for DNA helicase, complete cds.//6.30E-250//1426bp//88%/AB013912
 C-HEMBA1003392//Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.//0//1721bp//100%/AF074264
 50 C-HEMBA1003399//MVP1 PROTEIN.//2.30E-15//279aa//23%/P40959
 C-HEMBA1003487
 C-HEMBA1003530//S.scrofa mRNA for BM88 antigen.//1.20E-60//900bp//66%/X82027
 C-HEMBA1003602//Homo sapiens CGI-67 protein mRNA, complete cds.//3.50E-70//732bp//66%/AF151825
 55 C-HEMBA1003732//SFT2 PROTEIN.//1.50E-06//162aa//30%/P38166
 C-HEMBA1003945//Homo sapiens hypothetical 43.2 Kd protein mRNA, complete cds.//8.90E-287//757bp//97%/AF077030
 C-HEMBA1004110//Homo sapiens intersectin short form mRNA, complete cds.//0//2033bp//99%/AF064243

- C-HEMBA1004250//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//6.40E-51//277aa//35%//P33450
- C-HEMBA1004391//TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.//5.60E-20//194aa//26%//P70211
- C-HEMBA1004444//GLYCOPROTEIN 25L PRECURSOR (GP25L).//4.60E-41//148aa//52%//P27869
- 5 C-HEMBA1004454
- C-HEMBA1004505//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1 (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE).//2.70E-45//239aa//43%//P53624
- C-HEMBA1004797
- 10 C-HEMBA1004982//TETRACYCLINE RESISTANCE PROTEIN, CLASS E (TETA(E)).//6.30E-10//149aa//26%//Q07282
- C-HEMBA1005070//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.10E-05//187aa//29%//P17437
- C-HEMBA1005084//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PROTEIN KINASE 1).//1.20E-07//102aa//37%//P18160
- 15 C-HEMBA1005145
- C-HEMBA1005430
- C-HEMBA1005449//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//5.40E-10//224aa//24%//P13983
- C-HEMBA1005489
- 20 C-HEMBA1005522//COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).//7.70E-15//78aa//51%//P98139
- C-HEMBA1005545//MUSCARINIC ACETYLCHOLINE RECEPTOR M3.//0//2121aa//100%//U29589
- C-HEMBA1005698//Homo sapiens vesicle trafficking protein (SEC22C) mRNA, complete cds.//6.60E-163//753bp//99%//AF039568
- C-HEMBA1005913
- 25 C-HEMBA1005929//H.sapiens mRNA for serine/threonine protein kinase EMK.//6.50E-92//1092bp//69%//X97630
- C-HEMBA1005945//Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier mRNA, complete Gds.//1.90E-44//666bp//65%//AF004161
- C-HEMBA1006016
- C-HEMBA1006171
- 30 C-HEMBA1006299
- C-HEMBA1006311
- C-HEMBA1006335
- C-HEMBA1006430//Human putative transmembrane protein precursor (B5) mRNA, complete cds.//2.40E-70//1108bp//65%//L38961
- 35 C-HEMBA1006482//Homo sapiens h-scol (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//0//1101bp//98%//AF026852
- C-HEMBA1006572//ODD-SKIPPED PROTEIN.//2.60E-39//85aa//83%//P23803
- C-HEMBA1006707//Homo sapiens mRNA for matrilin-4, partial.//0//2003bp//99%//AJ007581
- C-HEMBA1006724
- 40 C-HEMBA1006902//Homo sapiens mRNA for matrilin-4, partial.//4.80E-275//1799bp//85%//AJ007581
- C-HEMBA1006916//Homo sapiens Grb14 mRNA, complete cds.//3.00E-277//1010bp//95%//L76687
- C-HEMBA1006960
- C-HEMBA1007013
- C-HEMBA1007057
- 45 C-HEMBA1007241
- C-HEMBA1007291
- C-HEMBA1007332
- C-HEMBA1000276
- C-HEMBA1000447//Homo sapiens JWA protein mRNA, complete cds.//0//2059bp//99%//AF070523
- 50 C-HEMBA1000642
- C-HEMBA1000668//Homo sapiens mRNA for KIAA0893 protein, complete cds.//0//2375bp//99%//AB020700
- C-HEMBA1000679//C.familiaris mRNA for TRAM-protein.//4.10E-210//1149bp//80%//X63678
- C-HEMBA1000881//Danio rerio mRNA for MINDIN2, complete cds.//1.70E-67//948bp//66%//AB006085
- C-HEMBA1000905//TRANSCRIPTIONAL REPRESSOR RCO-1.//1.00E-11//311aa//27%//P78706
- 55 C-HEMBA1001026//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT).//5.30E-11//142aa//30%//P32802
- C-HEMBA1001048//Human Hpast (HPAST) mRNA, complete cds.//6.50E-39//448bp//75%//AC000159

- C-HEMBB1001200
 C-HEMBB1001407
 C-HEMBB1001530//SLS1 PROTEIN PRECURSOR.//9.80E-10//273aa//27%//Q99158
 C-HEMBB1001573
 5 C-nnnnnnnnnnnn//Homo sapiens orphan G protein-coupled receptor (GPR34) gene, complete cds.//1.50E-251//
 1146bp//99%//AF118670
 C-HEMBB1001847//NEUROGENIC PROTEIN BIG BRAIN.//4.70E-06//258aa//24%//P23645
 C-HEMBB1001978
 C-HEMBB1002162//Homo sapiens genethonin 1 mRNA, complete cds.//8.30E-67//328bp//99%//AP062354
 10 C-HEMBB1002228
 C-HEMBB1002245//PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR
 (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN).//0//879aa//89%//Q62786
 C-HEMBB 1002427//FUCOSYLGLYCOPROTEIN ALPHA-N-ACETYL GALACTOSAMINYLTRANSFERASE (EC
 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3-AL-
 15 PHA-GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANS-
 FERASE) (NAGAT).//1.80E-70//221aa//50%//P16442
 C-HEMBB1002465//ACYL-COA DEHYDROGENASE (EC 1.3.99.-).//2.30E-53//249aa//48%//P45857
 C-HEMBB1002663
 C-HEMBB1002693
 20 C-MAMMA1000046
 C-MAMMA1000118
 C-nnnnnnnnnnnn//Homo sapiens SNC73 protein (SNC73) mRNA, complete cds.//1.50E-312//1594bp//93%//
 AF067420
 C-MAMMA1000449
 25 C-MAMMA1000457//Human NADH-cytochrome b5 reductase mRNA, 3' end.//9.50E-79//829bp//71%//M16462
 C-MAMMA1000591//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-
 UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYL GALACTOS-
 AMINYLTRANSFERASE) (GALNAC-T1).//1.20E-115//515aa//49%//Q07537
 C-MAMMA1000681//PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1.//9.40E-82//311aa//52%//O08530
 30 C-MAMMA1001043//MRC OX-45 SURFACE ANTIGEN PRECURSOR (BCM1 SURFACE ANTIGEN)(BLAST-1)
 (CD48).//2.90E-12//239aa//28%//P10252
 C-MAMMA1001893
 C-NT2RM2000241
 C-NT2RM2000306//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//4.50E-130//362aa//68%//P91917
 35 C-NT2RM2000410
 C-NT2RM2000423//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//1.80E-38//308aa//35%//
 P48982
 C-NT2RM2000497//CHL1 PROTEIN.//9.90E-24//296aa//29%//P22516
 C-NT2RM2000514//Homo sapiens mRNA for KIAA0875 protein, partial cds.//0//2381bp//99%//AB020682
 40 C-NT2RM2000622
 C-NT2RM2001126//Homo sapiens mRNA for multi PDZ domain protein.//0//1600bp//99%//AJ0001319
 C-NT2RM2001902//Homo sapiens mRNA for PAK4 protein.//5.40E-216//988bp//99%//AJ011855
 C-NT2RM2001939//Human G protein-coupled receptor GPR-NGA gene, complete cds.//0//1559bp//98%//U55312
 C-NT2RM2001941//MUSCARINIC ACETYLCHOLINE RECEPTOR M1.//7.40E-38//193aa//34%//P08482
 45 C-NT2RM4000198
 C-NT2RM4000284//Human IgG Fc receptor hFcRn mRNA, complete cds.//1.30E-257//603bp//96%//U12255
 C-NT2RM4000295
 C-NT2RM4000326//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//9.00E-100//434aa//43%//
 P51523
 50 C-NT2RM4000444//ANTIGEN PEPTIDE TRANSPORTER 1 (APT1).//1.70E-112//493aa//44%//P36370
 C-NT2RM4000587
 C-NT2RM4000648//K-GLYPICAN PRECURSOR.//4.00E-193//531aa//66%//P51655
 C-NT2RM4000997//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL).//1.80E-10//
 189aa//30%//P25234
 55 C-NT2RM4001321
 C-NT2RM4001325//CHONDROITIN 6-SULFOTRANSFERASE (EC 2.8.2.17) (C6ST).//2.90E-48//343aa//34%//
 Q92179
 C-NT2RM4001735

- C-NT2RM4002352//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds.//0//
2184bp//99%//AB009462
C-NT2RP1000002
C-NT2RP1000050
- 5 C-NT2RP1000181//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//3.30E-121//1394bp//69%//
AF126799
C-NT2RP1000261//ORM1 PROTEIN.//2.40E-17//137aa//35%//P53224
C-NT2RP1000300//Human transporter protein (g17) mRNA, complete cds.//3.80E-26//758bp//62%//U49082
C-NT2RP1000325//H.sapiens gene for phosphate carner.//0//439bp//98%//X77337
- 10 C-NT2RP1000448
C-NT2RP1000551//Homo sapiens putative interferon-related protein (SM15) mRNA, partial cds.//0//1761bp//
99%//U09585
C-NT2RP1000579//Human succinate dehydrogenase flavoprotein subunit (SDH) mRNA, complete cds.//0//
1951bp//94%//L21936
- 15 C-NT2RP1000613//CARBONIC ANHYDRASE VI (EC 4.2.1.1) (SALIVARY) (CARBONATE DEHYDRATASE VI).//
3.40E-52//304aa//40%//P08060
C-NT2RP1000903
C-NT2RP1000981//CELL SURFACE A33 ANTIGEN PRECURSOR.//3.60E-14//286aa//27%//Q99795
C-NT2RP1001004//F-SPONDIN PRECURSOR.//9.20E-43//322aa//35%//P35446
- 20 C-NT2RP1001020//SERINE/THREONINE-PROTEIN KINASE PAK-BETA (EC 2.7.1.-) (BETA-PAK) (P21-ACTI-
VATED KINASE 3) (CDC42/RAC EFFECTOR KINASE PAK-B).//9.70E-22//227aa//31%//Q61036
C-NT2RP1001563//TESTIS-SPECIFIC PROTEIN TPX-1 PRECURSOR (AUTOANTIGEN 1) (25 KD ACROSOM-
AL AUTOANTIGEN) (AA1).//9.70E-19//201aa//31%//Q60477
C-NT2RP2000394//Gallus gallus p52 pro-apototic protein mRNA, complete cds.//1.60E-90//956bp//70%//
AF029071
- 25 C-NT2RP2000479
C-NT2RP2000514//Homo sapiens roundabout 2 (robo2) mRNA, partial cds.//3.00E-185//855bp//99%//AF040991
C-NT2RP2000533//Homo sapiens cornichon protein mRNA, complete cds.//1.30E-290//1324bp//99%//AF070654
C-NT2RP2000649//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2847bp//99%//AB016068
- 30 C-NT2RP2000663
C-NT2RP2000694//Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.//0//2278bp//99%//AJ012159
C-NT2RP2000903//Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.//0//2276bp//100%//AJ012159
C-NT2RP2001480//Homo sapiens thrombospondin 3 (THBS3) gene, complete cds.//0//2547bp//99%//L38969
C-NT2RP2001495//Human transporter protein (g17) mRNA, complete cds.//2.20E-65//641bp//65%//U49082
- 35 C-NT2RP2001514//PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).//1.20E-133//429aa//
41%//P39986
C-NT2RP2001529//Homo sapiens mRNA for ZIP-kinase, complete cds.//0//2079bp//99%//AB007144
C-NT2RP2001769//SERINE/THREONINE-PROTEIN KINASE ORB6 (EC 2.7.1.-).//9.10E-47//185aa//44%//
O13310
- 40 C-NT2RP2001878
C-NT2RP2001903//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEU-
TRAL PROTEINASE) (CANP) (MU/M-TYPE).//3.80E-58//475aa//34%//P00789
C-NT2RP2001915
C-NT2RP2001956//ORM1 PROTEIN.//3.90E-19//137aa//37%//P53224
- 45 C-NT2RP2002063//GNS1 PROTEIN.//3.60E-18//231aa//33%//P25358
C-NT2RP2002188//Rattus norvegicus neuroligin 3 mRNA, complete cds.//2.50E-226//1284bp//89%//U41663
C-NT2RP2002232//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME 1.//1.90E-93//420aa//
43%//Q09782
- 50 C-NT2RP2002304//Human mRNA for KIAA0383 gene, partial cds.//0//1640bp//99%//AB002381
C-NT2RP2002409
C-NT2RP2002510
C-NT2RP2002527//CYTOCHROME B5.//1.30E-11//92aa//38%//P40312
C-NT2RP2002533//Homo sapiens alpha 2 delta calcium channel subunit isoform I mRNA, complete cds.//0//
2365bp//99%//AF042792
- 55 C-NT2RP2002564//Human zinc-finger protein C2H2-150 mRNA, complete cds.//0//2237bp//99%//U38864
C-NT2RP2002674//SOLUBLE EPOXIDE HYDROLASE (SEH) (EC 3.3.2.3) (EPOXIDE HYDRATASE) (CY-
TOSOLIC EPOXIDE HYDROLASE) (CEH).//5.50E-38//201aa//39%//P34913
C-NT2RP2002721//REGULATORY PROTEIN UHPC.//1.60E-23//153aa//30%//P27669

- C-NT2RP2002824//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHE-
ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENOCYTIC INTERMEDIATE COMPO-
NENT).//3.50E-63//404aa//33%//P32802
- 5 C-NT2RP2002942//Homo sapiens mRNA for KIAA0806 protein, complete cds.//0//2090bp//99%//AB018349
- C-NT2RP2002974//HOMEODOMAIN PROTEIN SIX5 (DM LOCUS-ASSOCIATED HOMEODOMAIN PROTEIN HO-
MOLOG) (FRAGMENT).//8.20E-241//555aa//84%//P70178
- C-NT2RP2002976
- 10 C-NT2RP2003042//PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43)
(LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE)
(FRAGMENT).//2.10E-109//385aa//52%//P53760
- C-NT2RP2003179//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1.-).//2.60E-67//256aa//
49%//Q05512
- C-NT2RP2003210//Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.//9.80E-272//1265bp//
98%//AF055899
- 15 C-NT2RP2003369//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//5.90E-20//204aa//
34%//Q15404
- C-NT2RP2003383//Homo sapiens mRNA for KIAA0458 protein, complete cds.//0//2565bp//99%//AB007927
- C-NT2RP2003469//GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).//1.10E-45//324aa//
29%//P37021
- 20 C-NT2RP2003545//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//5.40E-48//578bp//71%//
AF024636
- C-NT2RP2003593
- C-NT2RP2003599
- 25 C-NT2RP2003655//HYPOTHETICAL 26.3 KD PROTEIN IN OYE2-GND1 INTERGENIC//4.80E-15//93aa//47%//
P38869
- C-NT2RP2003931
- C-NT2RP2004141
- C-NT2RP2004179
- 30 C-NT2RP2004205//BUTYROPHILIN PRECURSOR (BT).//1.60E-21//276aa//32%//Q62556
- C-NT2RP2004447
- C-NT2RP2004495//Human transporter protein (g17) mRNA, complete cds.//9.80E-64//642bp//64%//U49082
- C-NT2RP2004524
- C-NT2RP2004556
- 35 C-NT2RP2004606//Human fibroblast collagenase inhibitor mRNA, complete cds.//2.10E-166//768bp//99%//
M12670
- C-NT2RP2004648//Mouse beta-galactosidase (BGAL) gene, complete cds.//1.20E-33//1136bp//59%//M57734
- C-NT2RP2004670//Rattus norvegicus vesicla-associate calmodulin-binding protein mRNA, complete cds.//0//
1250bp//86%//L22557
- 40 C-NT2RP2004794//HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.//2.70E-09//
203aa//26%//P40857
- C-NT2RP2004837
- C-NT2RP2004847//ZINC FINGER PROTEIN 135.//8.00E-35//193aa//40%//P52742
- C-nnnnnnnnnnnnn//Homo sapiens SCG10-like-protein (SCLIP) mRNA, complete cds.//2.90E-170//813bp//98%//
AF069709
- 45 C-NT2RP2005027
- C-NT2RP2005163
- C-NT2RP2005181//Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds.//5.30E-315//
2126bp//81%//U70859
- 50 C-NT2RP2005247//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//5.00E-53//296aa//37%//Q62158
- C-NT2RP2005425//Homo sapiens mRNA for AKAP450 protein.//0//4341bp//99%//AJ131693
- C-NT2RP2005463//PROTEIN PTM1 PRECURSOR.//7.40E-15//284aa//28%//P32857
- C-NT2RP2005514
- C-NT2RP2005541//N-ACETYLGLUCOSAMINE-6 SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLU-
COSAMINE-6-SULFATASE).//4.70E-24//78aa//51%//P15586
- 55 C-NT2RP2005632
- C-NT2RP2005878//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).//3.60E-55//238aa//50%//
O57314
- C-NT2RP2005883//DOPAMINE-BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA-

HYDROXYLASE) (DBH).//6.70E-72//512aa//34%//P15101
C-NT2RP2005887
C-NT2RP2005941//Human paired box gene (PAX6) homologue, complete cds.//1.40E-308//1396bp//99%//M93650

5 C-NT2RP2005994//HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.//3.50E-35//144aa//47%//P49191
C-NT2RP2006042//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.40E-15//501aa//25%//P08640
C-NT2RP2006269//DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 2 (E,C

10 2.4.1.109).//2.30E-78//679aa//32%//P31382
C-NT2RP2006512//GNS 1 PROTEIN.//2.00E-21//290aa//29%//P25358
C-NT2RP3000059//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//3.70E-12//133aa//32%//Q01485
C-NT2RP3000063//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//15 5.00E-29//596aa//30%//P19246
C-NT2RP3000125//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).//6.30E-08//70aa//41%//P29375
C-NT2RP3000169//Homo sapiens MRS1 mRNA, complete cds.//0//1519bp//97%//AF093239
C-NT2RP3000172//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).//1.30E-80//359aa//44%//Q14012

20 C-NT2RP3000201//Homo sapiens mRNA for KIAA0687 protein, partial cds.//2.00E-305//1224bp//99%//AB014587
C-NT2RP3000436//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.20E-27//90aa//42%//P38660
C-NT2RP3000460//Canis familiaris sec61 homologue mRNA, complete cds.//1.80E-198//643bp//89%//M96629
C-NT2RP3000616//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//5.20E-26//25 227aa//36%//Q06828
C-NT2RP3000721//HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION.//1.10E-22//171aa//36%//P38800
C-NT2RP3000820//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//1.90E-30//269aa//33%//P49695
C-NT2RP3000871

30 C-NT2RP3000907//PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).//2.20E-134//296aa//42%//P39986
C-NT2RP3001012//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//2906bp//98%//AB020636
C-NT2RP3001044
C-NT2RP3001061//Homo sapiens mRNA for KIAA0853 protein, partial cds.//0//3591bp//99%//AB020660
C-NT2RP3001170//Homo sapiens mRNA; cDNA DKFZp586K2120 (from clone DKFZp586K2120).//0//2421bp//99%//AL080163
C-NT2RP3001195//GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).//4.70E-48//339aa//29%//P37021

40 C-NT2RP3001240//Canis familiaris sec61 homologue mRNA, complete cds.//1.20E-301//1141bp//89%//M96629
C-NT2RP3001322//PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38) (ENDOPLASMIC RETICULUM CA²⁺-ATPASE).//1.70E-21//220aa//30%//P39524
C-NT2RP3001388//SYNAPTOTAGMIN IV.//2.00E-118//430aa//54%//P50232
C-nnnnnnnnnnnn//Human mRNA for KIAA0315 gene, partial cds.//0//2971bp//99%//AB002313
C-nnnnnnnnnnnn//Homo sapiens mRNA for KIAA0017 protein, complete cds.//0//3243bp//99%//D87686

45 C-NT2RP3001560//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//0//2468bp//99%//AF037339
C-NT2RP3001592//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC 2.1.1.32).//1.30E-18//279aa//27%//P15565
C-NT2RP3001738//CYTOCHROME B5.//1.30E-11//133aa//33%//P00169
C-NT2RP3001754
C-NT2RP3001858
C-NT2RP3002160//Canis familiaris forssman synthetase mRNA, complete cds.//5.00E-152//789bp//84%//U66140
C-NT2RP3002311//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//9.80E-103//547aa//43%//P48982

55 C-NT2RP3002342//Human transporter protein (g17) mRNA, complete cds.//1.70E-65//641bp//65%//U49082
C-NT2RP3002448
C-NT2RP3002721//Porcine citrate synthase mRNA, complete cds.//9.10E-281//1454bp//93%//M21197

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C-NT2RP3002738//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds.//2.20E-47//763bp//
 65%//L43821
 C-NT2RP3002790
 C-NT2RP3002836//Homo sapiens mRNA for KIAA0463 protein, partial cds.//0//1617bp//99%//AB007932
 5 C-NT2RP3002958//TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR.//
 8.00E-08//197aa//26%//P19814
 C-NT2RP3003000//Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds.//0//3160bp//
 96%//AF051946
 C-NT2RP3003076
 10 C-NT2RP3003354//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 3.//5.10E-55//208aa//51%//
 O35609
 C-NT2RP3003469
 C-NT2RP3003527//Homo sapiens mRNA for protein kinase Dyrk1B.//0//2483bp//99%//Y17999
 C-NT2RP3003535//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE
 15 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//8.80E-18//368aa//25%//P56558
 C-NT2RP3003559
 C-NT2RP3003614
 C-NT2RP3003729
 C-NT2RP3003849//PROTEIN KINASE C, BRAIN ISOZYME (EC 2.7.1.-) (PKC) (DPKC53E(BR)). PKC1.//1.20E-
 20 13//126aa//34%//P05130
 C-NT2RP3003874//Homo sapiens incomplete cDNA for a mutated allele of a myosin class I, myh-1c.//0//2160bp//
 98%//AJ001381
 C-NT2RP3003963
 C-NT2RP3004000
 25 C-NT2RP3004075
 C-NT2RP3004083
 C-NT2RP3004090//GOLIATH PROTEIN (G1 PROTEIN).//9.00E-33//179aa//47%//Q06003
 C-NT2RP3004130//CELL SURFACE ANTIGEN 114/A10 PRECURSOR.//8.10E-06//71aa//42%//P19467
 C-NT2RP3004133//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//2.50E-48//198aa//37%//P43636
 30 C-NT2RP3004202
 C-NT2RP3004309//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2584bp//
 99%//AL050118
 C-NT2RP3004321
 C-NT2RP3004355
 35 C-NT2RP3004374
 C-NT2RP3004406//HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION.//3.20E-15//
 165aa//33%//P40544
 C-NT2RP3004552//COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTI-
 GEN).//8.50E-24//263aa//33%//P17927
 40 C-NT2RP3004557//Human Ki nuclear autoantigen mRNA, complete cds.//0//2181bp//96%//U11292
 C-NT2RP3004625//Homo sapiens mRNA for KIAA0975 protein, partial cds.//0//1339bp//99%//AB023192
 C-NT2RP3004640//Bos taurus tuftelin mRNA, complete cds.//0//1204bp//88%//AF105228
 C-NT2RP3004647//PUTATIVE MITOCHONDRIAL CARRIER YMR166C.//2.00E-15//220aa//27%//Q03829
 C-NT2RP4000108//Human gene for neurofilament subunit NF-L.//0//1998bp//99%//AF176680
 45 C-NT2RP4000962//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//2.60E-18//225aa//32%//P08458
 C-NT2RP4001009//Homo sapiens mRNA for farnesylated-proteins converting enzyme 1.//0//2965bp//99%//
 Y13834
 C-NT2RP4001467//Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).//0//2140bp//99%//X55740
 C-OVARC1000090
 50 C-OVARC1000105//UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN
 LIGASE) (UBIQUITIN CARRIER PROTEIN).//4.20E-47//171aa//56%//P33296
 C-OVARC1000137
 C-OVARC1000208
 C-OVARC1000255//H.sapiens syk mRNA for protein-tyrosine kinase.//0//1525bp//97%//Z29630
 55 C-OVARC1000275//DESMOPLAKIN I AND II (DPI AND DPII) (FRAGMENT).//9.90E-16//352aa//23%//P15924
 C-OVARC1000298
 C-OVARC1000410//Homo sapiens angiopoietin Y1 mRNA, complete cds.//2.10E-63//744bp//69%//AF107253
 C-OVARC1000439//HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III.//1.40E-

33//143aa//53%/P34280
 C-OVARC1000467
 C-OVARC1000529//PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-)//1.40E-23//
 165aa//39%/P34244
 5 C-OVARC1000775
 C-nnnnnnnnnnnn//ZINC FINGER PROTEIN 157 //1.00E-35//130aa//46%/P51786
 C-OVARC1000811//PLASMINOGEN (EC 3.4.21.7) (FRAGMENT)//6.40E-13//115aa//34%/Q01177
 C-OVARC1000853
 C-OVARC1000916//H.sapiens PISSLRE mRNA //7.30E-280//1117bp//95%/X78342
 10 C-OVARC1000956//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN)//2.20E-09//250aa//
 28%/P17437
 C-OVARC1001030//Homo Sapiens mRNA for KIAA0886 protein, complete cds //0//907bp//99%/AB020693
 C-OVARC1001049//TRANSCRIPTION FACTOR HES- (C-HAIRY1)//7.50E-14//96aa//36%/O57337
 C-OVARC1001086//Homo Sapiens cyclin T2a mRNA, complete cds //0//1593bp//98%/AF048731
 15 C-OVARC10011321//GC-RICH SEQUENCE DNA-BINDING FACTOR (GCF) (TRANSCRIPTION FACTOR 9)
 (TCF-9)//2.30E-44//268aa//36%/P16383
 C-OVARC1001163//HYPOTHETICAL 49.3 KD PROTEIN C30D11.06C IN CHROMOSOME I//2.30E-20//152aa//
 30%/Q09906
 C-OVARC1001222
 20 C-OVARC1001338//AUTOPHAGY SERINE/THREONINE-PROTEIN KINASE APG1 (EC 2.7.1.-)//8.80E-30//
 125aa//40%/P53104
 C-OVARC1001569//PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-)//1.50E-22//
 164aa//39%/P34244
 C-OVARC1001596//Homo sapiens Arf-like 2 binding protein BART1 mRNA, complete cds //0//1766bp//99%/
 25 AF126062
 C-OVARC1001725
 C-OVARC1001727
 C-OVARC1001807//Human TR3 orphan receptor mRNA, complete cds //1.10E-243//1145bp//98%/L13740
 C-OVARC1001991//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID)//8.30E-06//114aa//
 30 35%/Q01956
 C-OVARC1002058//Human 18S rRNA gene, complete //1.50E-164//921bp//91%/M10098
 C-OVARC1002178
 C-PLACE1000033//VON WILLEBRAND FACTOR PRECURSOR//3.80E-17//190aa//28%/Q28295
 C-PLACE1000231//Rattus norvegicus WAP four-disulfide core domain protein (ps20) mRNA, complete cds //
 35 2.70E-101//947bp//74%/AF037272
 C-PLACE1000258//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7)//1.70E-55//431aa//
 35%/Q05481
 C-PLACE1000442//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)//1.00E-88//213aa//67%/P16415
 C-PLACE1000560
 40 C-PLACE1000740//Mus musculus (Notch2) mRNA, complete cds //5.60E-122//893bp//81%/M93661
 C-PLACE1000912
 C-PLACE1000914//Homo sapiens PB39 mRNA, complete cds //7.50E-88//500bp//69%/AF045584
 C-PLACE1000927//HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X//6.30E-21//123aa//
 37%/Q11079
 45 C-PLACE1001016//SODIUM CHANNEL PROTEIN PARA (PARALYTIC
 PROTEIN)//6.80E-12//133aa//28%/P35500
 C-nnnnnnnnnnnn//Homo sapiens T245 protein (T245) mRNA, complete cds //0//1801bp//99%/AF043906
 C-PLACE1001100
 C-PLACE1001114//HYPOTHETICAL BHLF1 PROTEIN//9.20E-06//389aa//31%/P03181
 50 C-PLACE1001123
 C-PLACE1001183
 C-PLACE1001229
 C-PLACE1001231//Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete
 cds //2.20E-137//918bp//80%/AF026554
 55 C-nnnnnnnnnnnn//Human pregnancy-specific beta 1-glycoprotein 4 (PSG4) clone FL-64 mRNA, complete cds //
 7.60E-293//1631bp//90%/U18469
 C-PLACE1001340//Homo sapiens mRNA for KIAA0719 protein, complete cds //0//2868bp//99%/AB018262
 C-PLACE1001401//HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGE

- FC RECEPTOR, BETA-SUBUNIT).//3.70E-18//148aa//39%/P13386
 C-PLACE1001407
 C-PLACE1001464//Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).//0//2756bp//99%/X55740
 C-PLACE1001500//Homo sapiens RecQ5 mRNA for DNA helicase, complete cds.//2.30E-27//1230bp//99%/
 5 AB006533
 C-PLACE1001516//240 KD PROTEIN OF ROD PHOTORECEPTOR CNG-CHANNEL [CONTAINS: GLUTAMIC
 ACID-RICH PROTEIN (GARP); CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4 (CNG CHANNEL 4) (CNG-
 4) (CYCLIC NUCLEOTIDE-GATED CATION CHANNEL MODULATORY SUBUNIT)].//2.30E-08//274aa//28%/
 Q28181
 10 C-PLACE1001536
 C-PLACE1001564//H.sapiens mRNA for HE6 Tm7 receptor.//5.10E-36//499bp//70%/X81892
 C-PLACE1001655//Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA, com-
 plete cds.//0//1708bp//99%/AF043472
 C-nnnnnnnnnnnn//Homo sapiens calumein (Calu) mRNA, complete cds.//0//1776bp//99%/AF013759
 15 C-PLACE1001788
 C-PLACE1001795//HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-SMC3 INTERGENIC REGION PRECUR-
 SOR.//3.40E-20//159aa//40%/P47032
 C-PLACE1001836//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEM-
 BRANE PROTEIN GP70; TRANSMEMBRANE PROTEIN P2OE].//5.00E-27//134aa//47%/P10269
 20 C-PLACE1001918//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHE-
 ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-
 NENT).//2.30E-53//339aa//33%/P32802
 C-PLACE1001949//PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).//3.00E-75//315aa//44%/
 Q12697
 25 C-PLACE1002080//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//0//1588bp//99%/AF039691
 C-PLACE1002095
 C-PLACE1002153//Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.//0//1202bp//99%/AF095791
 C-PLACE1002329//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//6.50E-105//
 213aa//45%/Q08509
 30 C-PLACE1002355//COMPLEMENT C4 PRECURSOR [CONTAINS: C4A ANAPHYLATOXIN].//4.20E-12//131aa//
 40%//P01029
 C-PLACE1002374//Human mRNA for pro-cathepsin L (major excreted protein MEP).//1.30E-313//1363bp//97%/
 X12451
 C-PLACE1002518
 35 C-PLACE1002547//Homo sapiens mRNA for KIAA0719 protein, complete cds.//0//2985bp//99%/AB018262
 C-PLACE1002726//Oryctolagus cuniculus mRNA for epithelial calcium channel (ECaC).//2.80E-202//926bp//
 82%/AJ133128
 C-PLACE1002905//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM
 BINDING INHIBITOR) (MA-DBI).//2.40E-37//188aa//40%/P07106
 40 C-PLACE1002911//POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR.//4.50E-39//345aa//32%/P32507
 C-PLACE1002967//HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCER1) (IGE
 FC RECEPTOR, BETA-SUBUNIT).//4.60E-08//156aa//30%/Q01362
 C-PLACE1003135//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//1.30E-47//210aa//49%/P08458
 C-PLACE1003163//Homo sapiens DBI-related protein mRNA, complete cds.//1.00E-294//1344bp//99%/
 45 AF069301
 C-PLACE1003428//Homo sapiens mRNA for VNN1 protein.//1.80E-142//676bp//72%/AJ132099
 C-PLACE1003438
 C-PLACE1003460
 C-PLACE1003529//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAG-
 50 MENT).//1.30E-09//281aa//22%/P11414
 C-PLACE1003573//T-CELL SURFACE GLYCOPROTEIN YE1/48 (T LYMPHOCYTE ANTIGEN A1) (LY49-A AN-
 TIGEN).//3.70E-16//226aa//26%/P20937
 C-PLACE1003598//TRP-ASP REPEATS CONTAINING PROTEIN RBA-1.//1.80E-07//161aa//27%/P90917
 C-PLACE1003644
 55 C-PLACE1003737//TOLL PROTEIN PRECURSOR.//5.40E-07//203aa//27%/P08953
 C-PLACE1003772//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//
 2.40E-12//124aa//38%/P 13983
 C-PLACE1003839//Homo sapiens putative G protein-coupled receptor (RAIG1) mRNA, complete cds.//8.10E-18//

- 771bp//58%//AF095448
 C-PLACE1003845//PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-
 GALACTOSE 4-EPIMERASE)//3.40E-37//302aa//30%//Q57664
 C-PLACE1003852//Homo sapiens mRNA for KIAA0758 protein, partial cds.//0//1667bp//99%//AB018301
 5 C-PLACE1004028
 C-PLACE1004166//CREB-BINDING PROTEIN.//1.80E-12//147aa//35%//P45481
 C-PLACE1004168//Homo sapiens mRNA for KIAA1007 protein, partial cds.//0//2637bp//99%//AB023224
 C-PLACE1004199
 C-PLACE1004279//HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III.//1.40E-08//166aa//
 10 30%//P30638
 C-PLACE1004282//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL)//2.10E-11//
 189aa//30%//P25234
 C-PLACE1004305//RAS-RELATED PROTEIN RAC1.//9.60E-29//197aa//41%//P40792
 C-PLACE1004441//Human G protein-coupled receptor (GPR1) gene, complete cds.//0//1880bp//98%//AC007383
 15 C-PLACE1004450//AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (LEUKEMIA AN-
 TIGEN CD13)//1.30E-91//562aa//35%//P15541
 C-PLACE 1004482//Rattus norvegicus hematopoietic lineage switch 2 related protein (Hls2-rp) mRNA, complete
 cds.//1.90E-246//1643bp//83%//AF097723
 C-PLACE1004519
 20 C-PLACE1004520//Human pregnancy-specific beta-glycoprotein d mRNA, complete cds.//9.10E-279//882bp//
 88%//M20881
 C-PLACE1004630
 C-PLACE1004637
 C-PLACE1004648//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
 25 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)//1.40E-18//395aa//25%//P08640
 C-nnnnnnnnnnnnn//Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.//0//1825bp//99%//
 AF049891
 C-PLACE1004816//Homo sapiens mRNA for Hakata antigen, complete cds.//1.00E-166//856bp//94%//D88587
 C-PLACE1004887//GOLIATH PROTEIN (G1 PROTEIN)//4.80E-33//179aa//47%//Q06003
 30 C-PLACE1005003//PROSTASIN PRECURSOR (EC 3.4.21.-)//2.20E-52//269aa//41%//Q16651
 C-PLACE1005005//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds.//4.10E-261//
 1209bp//98%//AF032456
 C-PLACE1005031//CHLORINE CHANNEL PROTEIN P64.//8.00E-92//205aa//87%//P35526
 C-PLACE1005239//Homo sapiens mRNA for HIRIP3 protein (clone pH4-31, pH4-17)//1.80E-235//1010bp//84%//
 35 AJ223351
 C-PLACE1005250//Homo sapiens D-type cyclin-interacting protein 1 (DIP1) mRNA, complete cds.//0//1046bp//
 96%//AF082569
 C-PLACE1005383//Homo sapiens UP50 mRNA, complete cds.//0//2019bp//99%//AF093118
 C-PLACE1005410//Canis familiaris sec61 homologue mRNA, complete cds.//2.40E-204//673bp//89%//M96629
 40 C-PLACE1005426//Human pregnancy-specific beta 1-glycoprotein 4 (PSG4) clone FL-64 mRNA, complete cds.//
 0//1629bp//95%//U18469
 C-PLACE1005519//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//4.60E-108//1070bp//73%//
 AF024636
 C-PLACE1005544//Mus musculus junctional adhesion molecule (Jam) mRNA, complete cds.//2.00E-159//
 45 1237bp//76%//U89915
 C-PLACE1005660//HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III.//1.90E-
 33//143aa//53%//P34280
 C-PLACE1005669
 C-PLACE1005682//B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN)//4.90E-09//183aa//33%//
 50 P20749
 C-PLACE1005725//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//7.60E-17//295aa//
 27%//Q11073
 C-PLACE1005736//Human mRNA for BAS-GRIP protein.//0//2378bp//99%//E16311
 C-PLACE1005768
 55 C-PLACE1005878//Bovine chlorine channel protein (p64) mRNA, complete cds.//5.90E-137//889bp//85%//L16547
 C-PLACE1006093
 C-PLACE1006208//Homo sapiens nGAP mRNA, complete cds.//3.30E-151//694bp//100%//AP047711
 C-PLACE1006219//PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-

GALACTOSE 4-EPIMERASE).//3.50E-37//302aa//30%//Q57664
 C-PLACE1006277//Homo sapiens mRNA for Z39lg protein.//0//1768bp//99%//AJ132502
 C-PLACE1006290//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.50E-75//301aa//39%//P43636
 C-PLACE1006443//Homo sapiens PB39 mRNA, complete cds.//4.30E-98//553bp//70%//AF045584
 5 C-PLACE1006515//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//2846bp//99%//AB011148
 C-PLACE1006716//30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADI-
 POCYTE SPECIFIC PROTEIN ADIPOQ).//4.60E-25//181aa//35%//Q60994
 C-PLACE1006809//SLS1 PROTEIN PRECURSOR.//9.10E-10//273aa//27%//P08124
 C-PLACE1006959
 10 C-PLACE1007028
 C-PLACE1007040
 C-PLACE1007096//PUTATIVE SUGAR TRANSPORT PROTEIN GETA.//2.70E-17//174aa//27%//O34368
 C-nnnnnnnnnnn//Homo sapiens mRNA for putative glucosyltransferase, partial cds.//0//1373bp//99%//AJ224875
 C-PLACE1007296//Human mRNA for a presumptive KDEL receptor.//1.10E-185//1038bp//91%//X55885
 15 C-PLACE1007591
 C-PLACE1007626//Homo sapiens unknown mRNA, complete cds.//3.00E-246//1122bp//99%//AF047439
 C-PLACE1007702//Mus musculus TRA1 mRNA, complete cds.//7.50E-41//662bp//64%//D78335
 C-PLACE1007845//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//4.80E-14//158aa//40%//P43636
 C-PLACE1007881//HYPOTHETICAL 69.4 KD PROTEIN F13H10.3 IN CHROMOSOME IV.//3.10E-99//504aa//
 20 42%//Q19425
 C-PLACE1008297//MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B).//1.30E-14//187aa//33%//
 P90648
 C-nnnnnnnnnnn//Homo sapiens mRNA for putative glucosyltransferase, partial cds.//0//1616bp//99%//AJ224875
 C-PLACE1008469
 25 C-PLACE1008549//Homo sapiens Ets transcription factor ESE-2b mRNA, complete cds.//0//2274bp//99%//
 AF115403
 C-PLACE1008657//Bovine mRNA for adseverin, complete cds.//7.80E-227//1246bp//90%//D26549
 C-PLACE1008716//Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.//0//
 1888bp//99%//U15128
 30 C-PLACE1008984
 C-PLACE1008985//Mus musculus synaptotagmin VIII mRNA, partial cds.//3.80E-140//650bp//81%//U20107
 C-PLACE1009067
 C-PLACE1009196
 C-PLACE1009279//cDNA encoding novel physiologically active protein which have serine protease activity.//
 35 6.60E-86//1414bp//64%//E12965
 C-PLACE1009527//Oryctolagus cuniculus mRNA for epithelial calcium channel (ECaC).//1.20E-87//585bp//83%//
 AJ133128
 C-PLACE1009546
 40 C-PLACE1009600//Mouse mRNA for tetracycline transporter-like protein, complete cds.//1.10E-264//924bp//
 88%//D88315
 C-PLACE1009735
 C-PLACE1009982//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//5.20E-08//166aa//28%//P02840
 C-PLACE1010078//ORM1 PROTEIN.//3.70E-19//137aa//37%//P53224
 C-PLACE1010081//Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.//0//2033bp//99%//
 45 AF027706
 C-PLACE1010251//FIBRILLIN 2 PRECURSOR.//1.70E-31//201aa//35%//Q61555
 C-PLACE1010784//Homo sapiens orphan G protein-coupled receptor (GPR34) gene, complete cds.//2.30E-252//
 1146bp//99%//AF008670
 C-PLACE1010827//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.90E-
 50 19//163aa//34%//P49020
 C-PLACE1010968//PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN- TY-
 ROSINE-PHOSPHATE PHOSPHOHYDROLASE).//3.40E-30//690aa//26%//P16621
 C-PLACE1011045//Homo sapiens E1-like protein mRNA, complete cds.//0//2376bp//99%//AF094516
 C-PLACE1011116//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE)
 55 (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//3.30E-09//234aa//27%//P08640
 C-PLACE1011236//Mus musculus mRNA for RST, complete cds.//1.70E-90//1398bp//65%//AB005451
 C-PLACE1011407//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.80E-133//342aa//59%//Q99676
 C-PLACE1011516//HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.//1.30E-13//

- 139aa//34%//P53073
 C-PLACE1011708//Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.//0//1840bp//98%//AF034611
 C-PLACE1011824//Human Ste20-like kinase (MST2) mRNA, complete cds.//6.40E-202//561bp//92%//U26424
 5 C-PLACE1011978//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-194//547aa//57%//Q05481
 C-PLACE2000118//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).//3.20E-27//205aa//43%//P70315
 C-PLACE2000219
 10 C-SKNMC1000004
 C-THYRO1000036//Homo sapiens collagen alpha 3 type IX (COL9A3) mRNA, complete cds.//1.20E-258//1376bp//93%//L41162
 C-THYRO1000061
 C-THYRO1000099
 15 C-THYRO1000196//Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds.//0//1632bp//91%//AF016272
 C-THYRO1000400//Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 25795.//0//1893bp//99%//AL109665
 C-THYRO1000580//ZINC FINGER PROTEIN 184 (FRAGMENT).//9.90E-114//279aa//59%//Q99676
 C-THYRO1000584//Homo sapiens mRNA for KIAA0935 protein, partial cds.//0//1338bp//99%//AB023152
 20 C-THYRO1000678//Homo sapiens Cx30 gene.//0//1741bp//97%//AJ005585
 C-THYRO1000795//C.elegans mRNA for Oxoglutarate/malate carrier protein.//8.80E-42//821bp//63%//X76114
 C-THYRO1000846
 C-THYRO1000866//SHK1 KINASE-BINDING PROTEIN 1.//4.40E-91//449aa//44%//P78963
 C-THYRO1000956//Human G protein-coupled receptor APJ gene, complete cds.//0//1583bp//99%//U03642
 25 C-THYRO1000999
 C-THYRO1001063
 C-THYRO1001071//GAMMA-ADAPTIN (GOLGI ADAPTOR HA1/AP1 ADAPTIN GAMMA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 GAMMA LARGE CHAIN).//8.20E-14//157aa//33%//P22892
 C-THYRO1001102
 30 C-THYRO1001113//Homo sapiens mRNA; cDNA DKFZp564E1616 (from clone DKFZp564E1616).//0//1361bp//99%//AL096713
 C-THYRO1001128
 C-THYRO1001205
 C-THYRO1001237//PHYTOENE DEHYDROGENASE (EC 1.3.-.-) (PHYTOENE DESATURASE) (ALBINO-1 PROTEIN).//3.10E-13//346aa//22%//P21334
 35 C-THYRO1001266//Human sodium iodide symporter mRNA, complete cds.//7.20E-81//1466bp//62%//U66088
 C-THYRO1001327
 C-THYRO1001456//HYPOTHETICAL 56.2 KD PROTEIN CY31.25C.//9.40E-32//355aa//31%//Q10555
 C-THYRO1001457//H.sapiens mRNA for protein kinase C mu.//2.30E-218//1183bp//73%//X75756
 40 C-THYRO1001471
 C-THYRO1001478//CYTOCHROME B-245 HEAVY CHAIN (P22 PHAGOCYTE B-CYTOCHROME) (NEUTROPHIL CYTOCHROME B, 91 KD POLYPEPTIDE) (CGD91-PHOX) (GP91-PHOX) (CYTOCHROME B(558) BETA CHAIN) (SUPEROXIDE-GENERATING NADPH OXIDASE HEAVY CHAIN SUBUNIT).//8.90E-50//296aa//35%//P04839
 45 C-THYRO1001495
 C-THYRO1001523//Homo sapiens mRNA for TM7XN1 protein.//0//3663bp//99%//AJ011001
 C-THYRO1001529//SERINE PALMITOYLTRANSFERASE 2 (EC 2.3.1.50) (LONG CHAIN BASE BIOSYNTHESIS PROTEIN 2) (SPT 2).//5.50E-25//115aa//53%//Q09925
 C-THYRO1001700//SERINE/THREONINE PROTEIN KINASE RIP (EC 2.7.1.-) (CELL DEATH PROTEIN RIP) (RECEPTOR INTERACTING PROTEIN).//9.70E-33//268aa//37%//Q60855
 50 C-THYRO1001702//Mus musculus mRNA for myeloid associated differentiation protein.//1.50E-128//1204bp//73%//AJ001616
 C-THYRO1001725
 C-THYRO1001803
 55 C-Y79AA1000127
 C-Y79AA1000207
 C-Y79AA1000226
 C-Y79AA1000270//Bos taurus vacuolar H+ ATPase subunit Ac45 mRNA, complete cds.//1.00E-271//1490bp//

- 83%/U10039
 C-Y79AA1000426/Mus musculus activin beta E subunit mRNA, complete cds.//7.70E-200//1533bp//78%/U96386
 C-Y79AA1000521
 C-Y79AA1000776
 5 C-Y79AA1000777//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.10E-48//283aa//38%/Q00808
 C-nnnnnnnnnnnn/Homo sapiens intersectin long form mRNA, complete cds.//0//1519bp//99%/AF064244
 C-Y79AA1000876//PROTEIN DISULFIDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72).//1.60E-44//210aa//38%/P13667
 C-Y79AA1000959//Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds.//4.80E-283//1405bp//95%/AF093420
 10 C-Y79AA1000967//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).//1.00E-77//359aa//44%/Q14012
 C-Y79AA1001013
 C-Y79AA1001056
 15 C-Y79AA1001062//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//8.90E-12//132aa//38%/Q13829
 C-Y79AA1001090//NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP-1) (NF-KAPPA-B1 P84/NF-KAPPA-B1 P98) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] (FRAGMENT).//4.50E-09//144aa//31 %//Q63369
 20 C-Y79AA1001264//HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR.//5.10E-106//351aa//58%/Q10005
 C-Y79AA1001272
 C-Y79AA1001328//Mus musculus mRNA for Dll3 protein, complete cds.//1.90E-263//1988bp//79%/AB013440
 C-Y79AA1001430//Homo sapiens mRNA for KIAA0469 protein, complete cds.//0//2943bp//99%/AB007938
 25 C-Y79AA1002022//POLIOVIRUS RECEPTOR HOMOLOG PECURSOR.//2.20E-06//140aa//26%/P32507
 C-BNGH41000020//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).//9.80E-159//347aa//90%/P03891
 C-BNGH41000091//POTASSIUM CHANNEL PROTEIN EAG.//1.20E-249//625aa//65%/Q02280
 C-HEMBA1000462//Human potential transcriptional repressor NOT4Hp (NOT4H) mRNA, complete cds.//0//935bp//99%/U71267
 30 C-HEMBA1000477//HYPOTHETICAL 64.8 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.//1.40E-38//344aa//34%/P40085
 C-HEMBA1000671//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.90E-104//388aa//46%/Q99676
 C-HEMBA1000732//Homo sapiens mRNA for latent transforming growth factor-beta binding protein-4.//0//2153bp//94%/Y13622
 35 C-HEMBA1000835
 C-HEMBA1000875
 C-HEMBA1001184//SH3BGR PROTEIN (21-GLUTAMIC ACID-RICH PROTEIN) (21-GARP).//2.50E-32//100aa//60%/P55822
 40 C-HEMBA1001272//Homo sapiens mRNA for KIAA1171 protein, partial cds.//0//1490bp//99%/AB032997
 C-HEMBA1001296
 C-HEMBA1002048//ODD-SKIPPED PROTEIN.//1.60E-55//122aa//75%/P23803
 C-HEMBA1002985
 C-HEMBA1003120//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.00E-193//547aa//54%/Q99676
 45 C-HEMBA1003497//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//4.00E-28//358aa//29%/Q60821
 C-HEMBA1004007
 C-HEMBA1004085
 C-HEMBA1004785//MODIFIER 3 PROTEIN (M33).//1.40E-27//221aa//33%/P30658
 50 C-HEMBA1004952
 C-HEMBA1004971
 C-HEMBA1005230//ZINC FINGER PROTEIN 140.//2.00E-17//83aa//66%/P52738
 C-HEMBA1005246
 C-HEMBA1005267//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN; NONERYTHROID).//8.40E-14//187aa//33%/Q01484
 55 C-HEMBA1006276//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).//1.70E-06//56aa//57%/Q61967
 C-HEMBA1006357//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.//3.70E-39//136aa//52%/

- O15127
 C-HEMBA1006517
 C-HEMBA1006544
 C-HEMBA1006749//Homo sapiens mRNA for matrilin-4, partial.//1.40E-275//1942bp//83%//AJ007581
 5 C-HEMBA1006770//FLOWERING TIME CONTROL PROTEIN FCA.//1.20E-33//352aa//34%//O04425
 C-HEMBA1006912
 C-HEMBA1007063
 C-HEMBB1000106//CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP).//1.60E-10//139aa//30%//P53996
 C-HEMBB1000407
 10 C-HEMBB1000542//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//2.60E-232//1452bp//85%//AF084259
 C-HEMBB1001547//Homo sapiens CGI-02 protein mRNA, complete cds.//0//2311bp//99%//AF132937
 C-HEMBB1001959//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//7.30E-14//97aa//38%//P25210
 15 C-HEMBB1002039
 C-HEMBB1002041//Homo sapiens transmembrane protein TENB2 (TENB2) mRNA, complete cds.//0//1746bp//99%//AF179274
 C-HEMBB1002051//Homo sapiens Ets transcription factor ESE-2b mRNA, complete cds.//1.30E-95//454bp//99%//AF115403
 20 C-HEMBB1002120//UDP-N-ACETYLGLUCOSAMINE-PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//4.90E-22//337aa//27%//P56558
 C-HEMBB1002302
 C-HEMBB1002661//Homo sapiens cardiovascular helix-loop-helix factor 2 (CHF2) mRNA, complete cds.//0//2174bp//99%//AF179274
 25 C-MAMMA1000106
 C-MAMMA1000141
 C-MAMMA1000204//Homo sapiens dysferlin mRNA, complete cds.//0//2028bp//99%//AF075575
 C-MAMMA1000226
 C-MAMMA1000403//Homo sapiens CDK4-binding protein p34SEI1 (SEI1) mRNA, complete cds.//1.20E-255//1165bp//99%//AF117959
 30 C-MAMMA1000473//HYPOTHETICAL 35.6 KD PROTEIN IN SPC1-ILV3 INTERGENIC REGION.//5.10E-45//299aa//34%//P47088
 C-MAMMA1000496//MIC1 PROTEIN.//3.00E-25//202aa//33%//P53258
 C-MAMMA1000528
 35 C-MAMMA1000614//Homo sapiens pseudouridine synthase 1 (PUS1) mRNA, partial cds.//2.10E-302//1370bp//99%//AF116238
 C-MAMMA1000652
 C-MAMMA1000706
 C-MAMMA1000788//Bos taurus P14 (p14) mRNA, complete cds.//3.90E-85//502bp//89%//AF037349
 40 C-MAMMA1000810
 C-MAMMA1000814
 C-MAMMA1000881//Homo sapiens protein kinase (SGK3) mRNA, complete cds.//0//1292bp//100%//AF169035
 C-MAMMA1000986
 C-MAMMA1000994//Homo sapiens ISLR(immunoglobulin superfamily containing leucine-rich repeat) mRNA, complete cds, alternatively spliced transcript ISLR-2.//0//2211bp//99%//AB024536
 45 C-MAMMA1001141
 C-MAMMA1001150//PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).//7.50E-304//587aa//68%//Q15139
 C-MAMMA1001237//MONOCARBOXYLATE TRANSPORTER 2 (MCT 2).//7.70E-64//196aa//41%//P53988
 C-MAMMA1001284
 50 C-MAMMA1001310//HYPOTHETICAL 57.3 KD TRP-ASP REPEATS CONTAINING PROTEIN IN POM152-REC114 INTERGENIC REGION.//1.50E-67//441aa//37%//Q04225
 C-MAMMA1001344
 C-MAMMA1001418//HYPOTHETICAL PROTEIN HI0519.//6.90E-27//181aa//38%//P44742
 C-MAMMA1001532//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.60E-126//319aa//56%//P51523
 55 C-MAMMA1001615//NEUROGENIC DIFFERENTIATION FACTOR 1.//3.80E-11//90aa//42%//Q13562
 C-MAMMA1001623//Homo sapiens mRNA; cDNA DKFZp434J1027 (from clone DKFZp434J1027); partial cds.//1.30E-269//1222bp//99%//AL133084

C-MAMMA1001634
 C-MAMMA1001957
 C-MAMMA1001978//Cimex lectularius apyrase (APY) mRNA, complete cds.//6.70E-19//988bp//56%//AF085499
 C-MAMMA1002070//PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).//1.10E-07//103aa//33%//Q01177
 5 C-MAMMA1002080//RAS-RELATED PROTEIN RAB-13.//1.80E-29//208aa//37%//P51153
 C-MAMMA1002087
 C-MAMMA1002095//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (P-TYPE CALCIUM ATPASE).//3.70E-22//867aa//52%//O43108
 C-MAMMA1002128//ABC1 PROTEIN HOMOLOG PRECURSOR.//2.50E-97//464aa//45%//Q92338
 10 C-MAMMA1002142//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).//9.80E-17//146aa//35%//P18160
 C-MAMMA1002165//Homo sapiens connective tissue growth factor related protein WISP-2 (WISP2) mRNA, complete cds.//4.80E-60//382bp//89%//AF100780
 C-MAMMA1002205//Homo sapiens mRNA; cDNA DKFZp586C091 (from clone DKFZp586C091).//2.00E-81//308bp//81%//AL050119
 15 C-MAMMA1002234//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//0//627aa//96%//Q00004
 C-MAMMA1002586//Homo sapiens alpha 1,2-mannosidase mRNA, complete cds.//0//2228bp//99%//AF148509
 C-MAMMA1002633
 C-MAMMA1003126//Human Hpast (HPAST) mRNA, complete cds.//3.70E-162//1355bp//75%//AF001434
 20 C-NT2RM1000580//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.50E-75//301aa//39%//P43636
 C-NT2RM1000858//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].//2.10E-98//1035bp//70%//S70011
 C-NT2RM2000565//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//9.40E-94//394aa//43%//Q09782
 C-NT2RM2000582//Homo sapiens mRNA for KIAA1053 protein, partial cds.//0//2666bp//99%//AB028976
 25 C-NT2RM2000589//Bos taurus myosin X, complete cds.//0//4376bp//84%//U55042
 C-NT2RM2000632//EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).//6.40E-62//183aa//47%//Q03468
 C-NT2RM2000773//Homo sapiens KNSL4 and MAZ genes for kinesin-like DNA binding protein and Myc-associated zinc finger protein, complete cds.//3.00E-289//1092bp//99%//AB017335
 30 C-NT2RM2001558//Homo sapiens protein kinase A binding protein AKAP110 mRNA, complete cds.//0//2398bp//99%//AF093408
 C-NT2RM2001626//FLIGHTLESS-1 PROTEIN HOMOLOG.//4.30E-19//362aa//26%//P34268
 C-NT2RM2001643
 C-NT2RM2001738//SOF1 PROTEIN.//3.00E-110//325aa//47%//P33750
 35 C-NT2RM2001792//Homo sapiens angiopoietin-related protein-2 mRNA, complete cds.//7.10E-149//995bp//86%//AF125175
 C-NT2RM2001818//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//4.30E-11//488aa//26%//P23253
 C-NT2RM4000100//Homo sapiens mRNA for KIAA0989 protein, partial cds.//0//2678bp//99%//AB023206
 40 C-NT2RM4000115//HYPOTHETICAL 68.8 KD PROTEIN B0464.6 IN CHROMOSOME III.//1.20E-16//204aa//30%//Q03564
 C-NT2RM4000417//SYNAPTOTAGMIN II.//2.70E-23//293aa//30%//P46097
 C-NT2RM4000593//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//3.90E-27//576aa//24%//Q10297
 45 C-NT2RM4000761//H.sapiens mitochondrial genome (consensus sequence).//0//1931bp//99%//X62996
 C-NT2RM4000965//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//9.00E-44//520aa//29%//O60100
 C-NT2RM4001377//Homo sapiens mRNA for KIAA0638 protein, partial cds.//0//1346bp//99%//AB014538
 C-NT2RM4001768//Homo sapiens CGI-82 protein mRNA, complete cds.//0//1925bp//99%//AF151840
 50 C-NT2RM4001843//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//6.20E-33//263aa//38%//P48982
 C-NT2RP1000239
 C-NT2RP1000465//UBIQUITIN-LIKE PROTEIN SMT3.//5.10E-07//81aa//33%//P55857
 C-NT2RP1000468//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//2.00E-13//97aa//38%//P25210
 55 C-NT2RP1000679
 C-NT2RP1000740//Homo sapiens mRNA; cDNA DKFZp586F1918 (from clone DKFZp586F1918).//4.60E-97//456bp//99%//AL050091

C-NT2RP1001031//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//3.40E-42//285aa//35%/Q00808
C-NT2RP2000178//MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//2.40E-192//
778aa//48%/P93647
C-NT2RP2000240
5 C-NT2RP2000447//GOLGIN-95.//2.80E-33//99aa//66%/Q08379
C-NT2RP2000610//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN
B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//1.50E-13//97aa//38%/P25210
C-NT2RP2000616//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//
10 4.10E-12//323aa//30%/P13983
C-NT2RP2000712//ZINC FINGER PROTEIN 135.//3.70E-87//296aa//53%/P52742
C-NT2RP2000739//ZINC FINGER PROTEIN 83 (ZNNC FNNGER PROTENN HPF1).//7.50E-73//387aa//37%/P
P51522
C-NT2RP2000818//Homo sapiens xenotropic and polytropic murine leukemia virus receptor (X3) mRNA, complete
cds.//0//2724bp//99%/AF089744
15 C-NT2RP2001200//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1539bp//100%/AB014576
C-NT2RP2001223//MYOTUBULARIN-RELATED PROTEIN 3 (FRAGMENT).//3.30E-05//76aa//39%/Q13615
C-NT2RP2001276//NPDC-1 PROTEIN PRECURSOR.//3.00E-133//331aa//77%/Q64322
C-NT2RP2001388//TRNA-SPUCING ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDO-
NUCLEASE).//5.90E-13//157aa//33%/P16658
20 C-NT2RP2001469//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.30E-14//242aa//24%/Q00808
C-NT2RP2001562//Homo Sapiens GLE1 (GLE1) mRNA, complete cds.//0//1899bp//98%/AF058922
C-NT2RP2001662//HOMEODOMAIN PROTEIN AKR (AVIAN KNOTTED-RELATED PROTEIN).//1.80E-49//
94aa//81%/Q90655
C-NT2RP2001755//Rattus norvegicus f-spondin mRNA, complete cds.//0//2974bp//86%/M88469
25 C-NT2RP2001817//Homo sapiens sirtuin type 1 (SIRT1) mRNA, complete cds.//0//3092bp//99%/AF083106
C-NT2RP2001948//HST2 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 2).//1.40E-08//191aa//27%/P53686
C-NT2RP2002015
C-NT2RP2003390//Homo sapiens mRNA for SEC63 protein.//0//2629bp//99%/AJ011779
C-NT2RP2003664//Homo sapiens mRNA for leptin receptor gene-related protein.//1.90E-237//1081bp//99%/Y
Y12670
30 C-NT2RP2003940//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//7.00E-111//401aa//43%/P28160
C-NT2RP2004069//HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME II.//3.00E-45//188aa//
52%/Q09297
C-NT2RP2004108//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.30E-171//474aa//62%/P16415
35 C-nnnnnnnnnnnn/Homo sapiens calumein (Calu) mRNA, complete cds.//0//2415bp//99%/AF013759
C-NT2RP2005069//Rat vacuolar protein sorting homolog r-vps33b mRNA, complete cds.//0//1792bp//87%/U
U35245
C-NT2RP2005378//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).//6.30E-
28//183aa//47%/P10496
40 C-NT2RP2005391//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor
Sp1.//0//1544bp//99%/AJ242978
C-NT2RP2005597//Homo sapiens protein O-mannosyl-transferase 1 (POMT1) mRNA, complete cds.//0//1821bp//
97%/AF095136
C-NT2RP2005666
45 C-NT2RP2006004//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//3.00E-26//
227aa//36%/Q06828
C-NT2RP2006092//Homo sapiens mRNA for Fe65L2, complete cds.//0//1156bp//99%/AB018247
C-NT2RP2006134
C-NT2RP3000011//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//4.00E-14//320aa//24%/Q00808
50 C-NT2RP3000022//Homo sapiens mRNA for KIAA0936 protein, complete cds.//0//2881bp//99%/AB023153
C-NT2RP3000171//Mus musculus partial mRNA for B-IND1 protein (B-ind1 gene).//4.40E-99//571bp//89%/Z
Z97207
C-NT2RP3000304//Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.//0//2895bp//99%/AF
AF074264
55 C-NT2RP3000378//PAIRED AMPHIPATHIC HELIX PROTEIN.//4.20E-39//186aa//36%/P22579
C-NT2RP3000444
C-NT2RP3000645
C-NT2RP3000676//PUTATIVE MITOCHONDRIAL CARRIER YMR166C.//2.10E-15//220aa//27%/Q03829

- C-NT2RP3000677//DNA BINDING PROTEIN RFX2.//3.60E-56//233aa//41%//P48378
 C-NT2RP3000789//Homo sapiens IGF-II mRNA-binding protein 1 (IMP-1) mRNA, complete cds.//0//1458bp//100%//AF117106
 C-NT2RP3000818
 5 C-NT2RP3000838//TRICHOHYALIN.//9.80E-11//491aa//26%//Q07283
 C-NT2RP3000921//TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR (COLORECTAL CANCER SUPPRESSOR).//4.00E-21//316aa//29%//P43146
 C-NT2RP3001159//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2558bp//99%//AL050118
 10 C-NT2RP3001271//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//2.60E-09//334aa//22%//P52178
 C-NT2RP3001542//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PROTEIN).//4.70E-11//132aa//37%//Q13829
 C-NT2RP3001685//PRPE PROTEIN.//1.00E-68//382aa//41%//P77495
 15 C-NT2RP3001976//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//8.90E-143//379aa//55%//P51523
 C-NT2RP3002015//Homo sapiens CGI-71 protein mRNA, complete cds.//0//1991bp//99%//AF151829
 C-NT2RP3002281//Homo sapiens mRNA for KIAA0765 protein, partial cds.//0//2286bp//99%//AB018308
 C-NT2RP3002286//Homo sapiens candidate tumor suppressor protein DICE 1 mRNA, complete cds.//0//2719bp//99%//AF097645
 20 C-NT2RP3002324
 C-NT2RP3002353
 C-NT2RP3002571//Homo sapiens mRNA for KIAA1108 protein, partial cds.//4.40E-273//1311bp//97%//AB029031
 C-NT2RP3002664
 25 C-NT2RP3002737//Homo sapiens voltage-gated potassium channel KCNQ4 (KCNQ4) mRNA, complete cds.//0//1552bp//99%//AF105202
 C-NT2RP3002887
 C-NT2RP3002900//Homo sapiens CGI-109 protein mRNA, complete cds.//8.70E-298//1321bp//92%//AF151867
 C-NT2RP3002983
 30 C-NT2RP3003473//Homo sapiens CGI-55 protein mRNA, complete cds.//5.50E-275//1309bp//98%//AF151813
 C-NT2RP3003532//OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (FRAGMENT).//4.40E-139//263aa//99%//P41217
 C-NT2RP3004025
 C-NT2RP3004067//Homo sapiens mRNA for NESCA, complete cds.//0//1962bp//99%//AB026894
 35 C-NT2RP3004119//PEREGRIN (BE140 PROTEIN).//7.30E-39//227aa//43%//P55201
 C-NT2RP3004294//Xenopus laevis ER1 mRNA, complete cds.//1.20E-71//335bp//79%//AF015454
 C-NT2RP3004345//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC 2.1.1.32).//3.90E-18//279aa//27%//P15565
 C-NT2RP4000634//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//0//1501bp//98%//AF111105
 40 C-NT2RP4001001//Homo sapiens clone 24856 mRNA sequence, complete cds.//3.90E-301//1374bp//99%//AF131856
 C-NT2RP4001877//Homo sapiens ribonucleoprotein RBM8 (RBM8) mRNA, complete cds.//0//2770bp//99%//AF127761
 45 C-NT2RP4001879
 C-NT2RP4002187//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2373bp//99%//AF078850
 C-NT2RP4002451
 C-NT2RP4002750//Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds.//1.00E-310//2084bp//81%//U70859
 50 C-OVARC1000003//Homo sapiens sodium dependent phosphate transporter isoform NaPi-3b mRNA, complete cds.//4.30E-220//1158bp//94%//AF111856
 C-OVARC1000313//Homo sapiens mRNA for KIAA0573 protein, partial cds.//0//1833bp//99%//AB011145
 C-OVARC1000331//GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE).//9.40E-44//106aa//59%//P36959
 55 C-OVARC1000553//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (THYMOCYTE-ACTIVATING MOLECULE) (THAM).//1.30E-23//169aa//40%//P28843
 C-OVARC1000873//Homo sapiens mRNA for KIAA1247 protein, partial cds.//0//2178bp//99%//AB033073

- C-OVARC1000995
C-OVARC1001260
C-OVARC1001336//Homo sapiens sodium dependent phosphate transporter isoform NaPi-3b mRNA, complete cds.//0//1435bp//99%//AF111856
- 5 C-OVARC1001570//Homo sapiens beta-site APP cleaving enzyme (BACE) mRNA, complete cds.//0//1792bp//100%//AF190725
C-OVARC1001607//Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.//0//1836bp//96%//U15128
- C-OVARC1001833//CIS-GOLGI MATRIX PROTEIN GM130.//6.60E-136//363aa//76%//Q62839
- 10 C-OVARC1001952//TRICHOHYALIN.//3.30E-16//487aa//27%//Q07283
C-PLACE1000986//Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817).//0//2055bp//99%//AL117450
C-PLACE1003407//Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds.//0//1965bp//99%//AF068227
- 15 C-PLACE1004078//Bovine mRNA for adseverin, complete cds.//0//2218bp//89%//D26549
C-PLACE1004492//VERPROLIN.//3.30E-07//149aa//29%//P37370
C-PLACE1005539//ACTIN POLYMERIZATION INHIBITOR (HEAT SHOCK 25 KD PROTEIN) (25-KD IAP).//3.10E-08//84aa//34%//Q00649
C-PLACE1005569//Homo sapiens mRNA for Z39lg protein.//0//1768bp//99%//AJ132502
- 20 C-PLACE1005601
C-PLACE1005745//ORM1 PROTEIN.//2.40E-17//137aa//35%//P53224
C-PLACE1005815//COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN).//1.50E-26//274aa//26%//P23508
C-PLACE1005927//HYPOTHETICAL 35.8 KD PROTEIN C12G12.12 IN CHROMOSOME I.//1.60E-38//333aa//33%//Q09875
- 25 C-PLACE1006071//LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN).//6.00E-08//215aa//26%//P02469
C-PLACE1006073//Homo sapiens mRNA for glucuronyltransferase I, complete cds.//4.10E-316//1020bp//96%//AB009598
- 30 C-PLACE1006079//Homo sapiens distal-less homeobox protein (DLX3) gene, complete cds.//0//1379bp//97%//AF028233
C-PLACE1006786
C-PLACE1007077//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//2578bp//99%//AB023194
C-PLACE1007971
- 35 C-PLACE1008282//HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-) (HRI).//7.10E-274//627aa//82%//P33279
C-PLACE1008359//BEM46 PROTEIN (FRAGMENT).//1.70E-50//289aa//42%//P54069
C-PLACE1008744//Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 248114.//0//1757bp//99%//AL079279
- 40 C-PLACE1010445
C-PLACE1010713//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2374bp//99%//AF078850
C-nnnnnnnnnnnnn//Homo sapiens angiopoietin-2 mRNA, complete cds.//0//2227bp//99%//AF004327
C-PLACE1011181//MSP1 PROTEIN HOMOLOG.//9.40E-82//353aa//47%//P54815
- 45 C-PLACE1011364//MYOTONIN-PROTEIN KINASE (EC 2.7.1.-) (MYOTONIC DYSTROPHY PROTEIN KINASE) (MDPK) (DM-KINASE) (DMK) (DMPK) (MT-PK).//2.20E-09//153aa//32%//Q09013
C-PLACE3000181//Human protocadherin 42 mRNA, complete cds for abbreviated PC42.//0//2719bp//95%//L11370
C-SKNMC1000014
- 50 C-SKNMC1000082//BRITTLE-1 PROTEIN PRECURSOR.//3.70E-31//307aa//30%//P29518
C-THYRO1000964
C-THYRO1001242//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//0//2468bp//99%//AF037339
C-THYRO1001608
- 55 C-THYRO1001641//Homo sapiens CGI-57 protein mRNA, complete cds.//0//1668bp//99%//AF151815
C-THYRO1001770//PROBABLE SERINE/THREONINE-PROTEIN KINASE YNL020C (EC 2.7.1.-).//6.30E-20//1169aa//35%//P53974
C-Y79AA1000030//Homo sapiens mRNA for Fe65L2, complete cds.//0//1828bp//100%//AB018247

- C-Y79AA1001212//Homo sapiens SL15 protein mRNA, complete cds.//6.30E-306//1388bp//99%//AF038961
 C-Y79AA1001426//ANION EXCHANGE PROTEIN 3 (CARDIAC/BRAIN BAND 3-LIKE PROTEIN) (CAE3/BAE3).//
 6.20E-66//609aa//31%//P48751
 5 C-Y79AA1001427//Homo sapiens cytochrome b5 reductase 1 (B5R.1) mRNA, complete cds.//0//1588bp//99%//
 AF169481
 C-Y79AA1001523//Homo sapiens transcriptional intermediary factor 1 alpha mRNA, complete cds.//0//2263bp//
 99%//AF119042
 C-Y79AA1001530//Human beta-tubulin gene (5-beta) with ten Alu family members.//0//1920bp//98%//X00734
 C-Y79AA1001592
 10 C-Y79AA1001727//CELL SURFACE A33 ANTIGEN PRECURSOR.//1.10E-13//286aa//27%//Q99795
 C-Y79AA1001787//PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).//1.70E-133//544aa//37%//
 Q12697
 C-Y79AA1001793//Mus musculus mRNA for GSG1, complete cds.//3.70E-126//532bp//78%//D87325
 C-Y79AA1001795//Homo sapiens mRNA for GalT4 protein.//2.30E-250//1137bp//99%//Y15061
 15 C-Y79AA1001799//MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.//3.40E-54//182aa//39%//P23500
 C-Y79AA1001803//Homo sapiens secretogranin III mRNA, complete cds.//0//1871bp//99%//AF078851
 C-Y79AA1001863
 C-Y79AA1002058//Mus musculus Gng31g mRNA, complete cds.//4.10E-167//1145bp//83%//AF069954
 C-Y79AA1002121//HISTONE H1.//4.90E-12//114aa//35%//P35060
 20 C-Y79AA1002213//HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III.//1.20E-98//262aa//
 41%//Q03567
 C-Y79AA1002373//Mus musculus mRNA for GSG1, complete cds.//7.20E-147//680bp//79%//D87325
 C-Y79AA1002376//Rattus norvegicus cytoplasmic dynein intermediate chain 2B mRNA, complete cds.//1.50E-
 304//1667bp//90%//U39045
 25 C-Y79AA1002378//Homo sapiens zinc finger protein NY-REN-21 antigen mRNA, partial cds.//0//963bp//99%//
 AF155100
 C-Y79AA1002381//Homo sapiens cell cycle related kinase mRNA, complete cds.//0//1791bp//98%//AF035013
 C-BNGH41000087//Homo sapiens mRNA for KIAA1247 protein, partial cds.//0//2294bp//99%//AB033073
 C-HEMBA1001886
 30 C-HEMBA1004067//Homo sapiens mRNA for KIAA0859 protein, complete cds.//8.30E-309//623bp//99%//
 AB020666
 C-HEMBA1007226//Homo sapiens RPA-binding trans-activator (RBT1) mRNA, complete cds.//7.30E-273//
 1242bp//99%//AF192529
 C-HEMBB1000309
 35 C-HEMBB1000567
 C-MAMMA1000102//APOLIPOPROTEIN L PRECURSOR (APO-L).//1.40E-21//221aa//35%//O14791
 C-MAMMA1001066
 C-MAMMA1001094//Human potential transcriptional repressor NOT4Hp (NOT4H) mRNA, complete cds.//0//
 1394bp//93%//U71267
 40 C-MAMMA1001609
 C-MAMMA1001901
 C-MAMMA1002091//Homo sapiens CD39L2 (CD39L2) mRNA, complete cds.//0//2564bp//99%//AF039916
 C-NT2RM1000462
 C-NT2RM1000542//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//1.40E-103//566aa//
 45 43%//P48982
 C-NT2RM1000789//Homo sapiens mRNA for hTCF-4.//2.80E-221//757bp//99%//Y11306
 C-NT2RM1000855//Homo sapiens sec61 homolog mRNA, complete cds.//0//3541bp//99%//AF084458
 C-NT2RM1000899//MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.//1.10E-54//182aa//39%//P23500
 C-NT2RP2000092//ZINC FINGER PROTEIN 136.//1.90E-117//419aa//54%//P52737
 50 C-NT2RP2001538//Homo sapiens mRNA; cDNA DKFZp434K2235 (from clone DKFZp434K2235).//0//2139bp//
 99%//AL117513
 C-NT2RP2001921
 C-NT2RP2003138//5'-TG-3'INTERACTING FACTOR (HOMEBOX PROTEIN TGIF).//2.10E-08//104aa//46%//
 P70284
 55 C-NT2RP2003302//Homo sapiens GIOT-4 mRNA for gonadotropin inducible transcription repressor-4, complete
 cds.//0//2891bp//99%//AB021644
 C-NT2RP2003950//Homo sapiens clone 24778 unknown mRNA.//0//1545bp//99%//AF070572
 C-NT2RP2005535//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.90E-172//489aa//

62%//Q03923
 C-NT2RP2005774//Homo sapiens GIOT-4 mRNA for gonadotropin inducible transcription repressor-4, complete cds.//6.90E-224//1461bp//72%//AB021644
 C-NT2RP3000148//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//4.10E-106//350aa//47%//
 5 P51523
 C-NT2RP3000232//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.40E-130//693aa//41%//Q99676
 C-NT2RP3000427
 C-NT2RP3000652//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.90E-153//441aa//62%//P28160
 C-NT2RP3001650//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).//2.20E-22//
 10 107aa//42%//P98063
 C-NT2RP3002409//Homo sapiens mRNA for KIAA0719 protein, complete cds.//0//2404bp//99%//AB018262
 C-NT2RP3002411//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2374bp//99%//
 AF078850
 C-NT2RP3003448
 15 C-NT2RP4002715
 C-OVARC1000307//HYPOTHETICAL 29.7 KD PROTEIN CY339.02.//3.00E-19//194aa//35%//Q50658
 C-PLACE1000907//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.30E-204//396aa//85%//
 P51522
 C-PLACE1007081
 20 C-PLACE1010011//Homo sapiens AAPT1-like protein mRNA, partial cds.//1.70E-237//1092bp//99%//AF047431
 C-PLACE3000213//COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR).//4.60E-68//317aa//34%//P19070
 C-PLACE4000354//COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).//1.00E-129//482aa//29%//P17927
 25 C-PLACE4000455
 C-THYRO1000776//PROBABLE SULFATE PERMEASE SPBC3H7.02.//1.30E-68//442aa//36%//O74377
 C-THYRO1001593//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//3.10E-203//550aa//
 62%//P27448
 C-Y79AA1000750
 30 C-Y79AA1000888//TRNA PSEUDOURIDINE SYNTHASE A (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE I) (PSEUDOURIDINE SYNTHASE I) (URACIL HYDROLYASE).//1.50E-21//267aa//32%//P70973
 C-Y79AA1002129
 C-Y79AA1002334//GLUCOSE REPRESSION MEDIATOR PROTEIN.//1.70E-10//333aa//23%//P14922
 C-BNGH41000020//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).//9.80E-159//347aa//90%//
 35 P03891
 C-BNGH41000087//N-ACETYLGUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).//1.20E-17//83aa//40%//P50426
 C-BNGH41000091//POTASSIUM CHANNEL PROTEIN EAG.//1.20E-249//625aa//65%//Q02280
 C-HEMBA1000006//Homo sapiens mRNA for NESCA, complete cds.//0//1230bp//92%//AB026894
 40 C-HEMBA1000121//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III.//4.80E-05//83aa//27%//
 P34679
 C-HEMBA1000128//PATHOGENESIS-RELATED PROTEIN 1 PRECURSOR (PR-1).//3.20E-07//89aa//34%//
 P33154
 C-HEMBA1000275
 45 C-HEMBA1000300
 C-HEMBA1000349//ATP-BINDING CASSETTE TRANSPORTER 1.//5.30E-65//352aa//39%//P41233
 C-HEMBA1000443//Homo sapiens CGI-96 protein mRNA, complete cds.//4.70E-129//686bp//91%//AF151854
 C-HEMBA1000462//Human potential transcriptional repressor NOT4Hp (NOT4H) mRNA, complete cds.//0//
 935bp//99%//U71267
 50 C-HEMBA1000477//HYPOTHETICAL 64.8 KD PROTEIN IN GDI1-COX15 INTERGENIC REGION.//1.40E-38//
 344aa//34%//P40085
 C-HEMBA1000590//Homo sapiens mRNA for matrilin-4, partial.//2.00E-273//1254bp//99%//AJ007581
 C-HEMBA1000634//Homo sapiens T-cell activation protein (PGR1) gene, complete cds.//0//994bp//99%//
 AF116272
 55 C-HEMBA1000671//ZINC FINGER. PROTEIN 184 (FRAGMENT).//3.90E-104//388aa//46%//Q99676
 C-HEMBA1000713//Homo sapiens 10kD protein (BC10) mRNA, complete cds.//0//1254bp//99%//AF053470
 C-HEMBA1000732//Homo sapiens mRNA for latent transforming growth factor-beta binding protein-4.//0//
 2153bp//94%//Y13622

- C-HEMBA1000745//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//2.00E-07//445aa//27%//P02454
 C-HEMBA1000835//FIBRILLIN 2 PRECURSOR.//1.30E-42//214aa//45%//P35556
 C-HEMBA1000875
 C-HEMBA1000907
 5 C-HEMBA1000940//GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44).//2.90E-39//362aa//31%//P41987
 C-HEMBA1000962
 C-HEMBA1001184//SH3BGR PROTEIN (21-GLUTAMIC ACID-RICH PROTEIN) (21-GARP).//2.50E-32//100aa//60%//P55822
 10 C-HEMBA1001221//AGRIN PRECURSOR.//2.50E-25//294aa//29%//P31696
 C-HEMBA1001228//Human germline oligomeric matrix protein (COMP) mRNA, complete cds.//7.80E-286//1105bp//94%//L32137
 C-HEMBA1001272//Homo sapiens mRNA for KIAA1171 protein, partial cds.//0//1490bp//99%//AB032997
 C-HEMBA1001296
 15 C-HEMBA1001297//Homo sapiens putative transcription factor CA150 mRNA, complete cds.//4.60E-276//1081bp//99%//AF017789
 C-HEMBA1001390//Mus musculus polymerase I-transcript release factor mRNA, complete cds.//2.50E-57//464bp//82%//AF036249
 C-HEMBA1001563
 20 C-HEMBA1001621//PROBABLE G PROTEIN-COUPLED RECEPTOR APJ.//3.50E-123//259aa//89%//P35414
 C-HEMBA1001878//Homo sapiens U5 snRNP-specific 40 kDa protein mRNA, complete cds.//0//1488bp//99%//AF090988
 C-HEMBA1001886//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.40E-148//421aa//60%//Q03923
 25 C-HEMBA1002048//ODD-SKIPPED PROTEIN.//1.60E-55//122aa//75%//P23803
 C-HEMBA1002131//PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1//4.10E-10//140aa//30%//P24802
 C-HEMBA1002163//HYPOTHETICAL 40.7 KD PROTEIN IN DAK1-ORC1 INTERGENIC REGION.//9.40E-28//309aa//30%//Q04651
 30 C-HEMBA1002164
 C-HEMBA1002167//Rattus norvegicus neuroligin I mRNA, complete cds.//1.30E-305//1643bp//91%//U22952
 C-HEMBA1002178//PROCOLLAGEN-LYSINE,2-OXOGLUTARATE 5-DIOXYGENASE 1 PRECURSOR (EC 1.14.11.4) (LYSYL HYDROXYLASE 1) (LH1).//3.70E-10//140aa//30%//P24802
 C-HEMBA1002195//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.80E-23//221aa//31%//Q00808
 35 C-HEMBA1002227//Homo sapiens mRNA for 80K-L protein, complete cds.//0//1324bp//98%//D10522
 C-HEMBA1002239
 C-HEMBA1002316//GTP-BINDING PROTEIN HFLX.//5.80E-12//196aa//29%//P25519
 C-HEMBA1002420
 40 C-HEMBA1002421//Human heparan sulfate proteoglycan (HSPG) core protein, 3' end.//0//2097bp//99%//J04621
 C-HEMBA1002524//Human MHC Class I region proline rich protein mRNA, complete cds.//0//1763bp//95%//U63336
 C-HEMBA1002551//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//9.80E-08//110aa//37%//P49695
 C-HEMBA1002767//Homo sapiens chromosome 1p33-p34 beta-1,4-galactosyltransferase mRNA, complete cds.//0//1497bp//99%//AF038660
 45 C-HEMBA1002985
 C-HEMBA1002992//UBIQUITIN-LIKE PROTEIN DSK2.//2.00E-21//216aa//35%//P48510
 C-HEMBA1003047//Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.//0//1768bp//99%//AF034611
 50 C-HEMBA1003072//Gallus gallus single-strand DNA-binding protein csdp mRNA, partial cds.//3.30E-93//927bp//73%//U68380
 C-HEMBA1003101//Homo sapiens tyrosylprotein sulfotransferase-2 mRNA, complete cds.//0//1854bp//99%//AF049891
 C-HEMBA1003120//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.00E-193//547aa//54%//Q99676
 55 C-HEMBA1003230//Homo sapiens fibulin-5.//5.60E-308//1398bp//99%//AJ133490
 C-HEMBA1003294
 C-HEMBA1003315//Mus musculus mRNA for DNA helicase, complete cds.//6.30E-250//1426bp//88%//AB013912
 C-HEMBA1003392//Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.//0//1721bp//

100%//AF074264
 C-HEMBA1003399//MVP1 PROTEIN.//2.30E-15//279aa//23%//P40959
 C-HEMBA1003487
 5 C-HEMBA1003497//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING
 PROTEIN) (LP-1) (ZINC FINGER PROTEIN Z13).//4.00E-28//358aa//29%//Q60821
 C-HEMBA1003530//S.scrofa mRNA for BM88 antigen.//1.20E-60//900bp//66%//X82027
 C-HEMBA1003602//HYPOTHETICAL 29.7 KD PROTEIN CY339.02.//2.80E-21//200aa//33%//Q50658
 C-HEMBA1003732//SFT2 PROTEIN.//1.50E-06//162aa//30%//P38166
 10 C-HEMBA1003945//Homo sapiens hypothetical 43.2 Kd protein mRNA, complete cds.//8.90E-287//757bp//97%//
 AF077030
 C-HEMBA1004007
 C-HEMBA1004067//Homo sapiens mRNA for KIAA0859 protein, complete cds.//0.00E+00//623bp//99%//
 AB020666
 C-HEMBA1004085
 15 C-HEMBA1004110//Homo sapiens intersectin short form mRNA, complete cds.//0//2033bp//99%//AF064243
 C-HEMBA1004250//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT PROTEIN).//6.40E-51//
 277aa//35%//P33450
 C-HEMBA1004391//TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR.//5.60E-20//194aa//26%//F70211
 C-HEMBA1004444//GLYCOPROTEIN 25L PRECURSOR (GP25L).//4.60E-41//148aa//52%//P27869
 20 C-HEMBA1004454
 C-HEMBA1004505//MANNOSYL-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE ISOFORM 1 (EC
 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE).//2.70E-45//239aa//43%//P53624
 C-HEMBA1004785//MODIFIER 3 PROTEIN (M33).//1.40E-27//221aa//33%//P30658
 C-HEMBA1004797
 25 C-HEMBA1004952
 C-HEMBA1004971
 C-HEMBA1004982//TETRACYCLINE RESISTANCE PROTEIN, CLASS E (TETA(E)).//6.30E-10//149aa//26%//
 Q07282
 C-HEMBA1005070//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.10E-05//187aa//
 30 29%//P17437
 C-HEMBA1005084//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-
 TEIN KINASE 1).//1.20E-07//102aa//37%//P18160
 C-HEMBA1005145
 C-HEMBA1005230//ZINC FINGER PROTEIN 140.//2.00E-17//83aa//66%//P52738
 35 C-HEMBA1005246//HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 4 (HFH-4).//2.10E-15//
 230aa//28%//Q92949
 C-HEMBA1005267//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NONERYTHROID).//8.40E-14//
 187aa//33%//Q01484
 C-HEMBA1005430
 40 C-HEMBA1005449//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//
 5.40E-10//224aa//24%//P13983
 C-HEMBA1005489//Mus musculus semaphorin cytoplasmic domain-associated protein 3A (Semcap3) mRNA,
 complete cds.//8.40E-255//924bp//80%//AF127084
 C-HEMBA1005522//COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).//7.70E-15//78aa//51%//P98139
 45 C-HEMBA1005545//MUSCARINIC ACETYLCHOLINE RECEPTOR M3.//0//590aa//100%//P20309
 C-HEMBA1005698//Homo sapiens vesicle trafficking protein (SEC22C) mRNA, complete cds.//6.60E-163//
 753bp//99%//AF039568
 C-HEMBA1005913
 C-HEMBA1005929//H.sapiens mRNA for serine/threonine protein kinase EMK.//6.50E-92//1092bp//69%//X97630
 50 C-HEMBA1005945//BRITTLE-1 PROTEIN PRECURSOR.//1.70E-29//220aa//35%//P29518
 C-HEMBA1006016
 C-HEMBA1006171
 C-HEMBA1006276//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).//1.70E-06//56aa//
 57%//Q61967
 55 C-HEMBA1006299
 C-HEMBA1006311
 C-HEMBA1006335
 C-HEMBA1006357//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 2.//3.70E-39//136aa//52%//

O15127
 C-HEMBA1006430//Human putative transmembrane protein precursor (B5) mRNA, complete cds.//2.40E-70//
 1108bp//65%//L38961
 C-HEMBA1006482//Homo sapiens h-sco1 (SCO1) mRNA, nuclear gene encoding mitochondrial protein, complete
 5 cds.//0//1101bp//98%//AF026852
 C-HEMBA1006517
 C-HEMBA1006544
 C-HEMBA1006572//ODD-SKIPPED PROTEIN.//2.60E-39//85aa//83%//P23803
 C-HEMBA1006658//Homo sapiens mRNA for NIK, partial cds.//0//1500bp//98%//AB013385
 10 C-HEMBA1006707//Homo sapiens mRNA for matrilin-4, partial.//0//2003bp//99%//AJ007581
 C-HEMBA1006724
 C-HEMBA1006749//Homo sapiens mRNA for matrilin-4, partial.//1.40E-275//1942bp//83%//AJ007581
 C-HEMBA1006770//FLOWERING TIME CONTROL PROTEIN FCA.//1.20E-33//352aa//34%//O04425
 C-HEMBA1006902//Homo sapiens mRNA for matrilin-4, partial.//4.80E-275//1799bp//85%//AJ007581
 15 C-HEMBA1006912
 C-HEMBA1006916//Homo sapiens Grb14 mRNA, complete cds.//3.00E-277//1010bp//95%//L76687
 C-HEMBA1006960
 C-HEMBA1007013//Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds.//1.10E-14//412bp//63%//
 AF068749
 20 C-HEMBA1007057
 C-HEMBA1007063
 C-HEMBA1007226//Homo sapiens RPA-binding trans-activator (RBT1) mRNA, complete cds.//7.30E-273//
 1242bp//99%//AF192529
 C-HEMBA1007241//HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.//2.70E-14//
 25 106aa//42%//P40857
 C-HEMBA1007291
 C-HEMBA1007332//Homo sapiens mRNA for unr-interacting protein.//6.40E-83//266bp//98%//AJ010025
 C-HEMBA1000106//CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP).//1.60E-10//139aa//30%//P53996
 C-HEMBA1000276
 30 C-HEMBA1000309
 C-HEMBA1000407
 C-HEMBA1000447//Homo sapiens JWA protein mRNA, complete cds.//0//2059bp//99%//AF070523
 C-HEMBA1000542//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//2.60E-232//
 1452bp//85%//AF084259
 35 C-HEMBA1000567
 C-HEMBA1000642
 C-HEMBA1000668//Homo sapiens mRNA for KIAA0893 protein, complete cds.//0//2375bp//99%//AB020700
 C-HEMBA1000679//C.familiaris mRNA for TRAM-protein.//4.10E-210//1149bp//80%//X63678
 C-HEMBA1000881//Danio rerio mRNA for MINDIN2, complete cds.//1.70E-67//948bp//66%//AB006085
 40 C-HEMBA1000905//TRANSCRIPTIONAL REPRESSOR RCO-1.//1.00E-11//311aa//27%//P78706
 C-HEMBA1001026//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENOMEMBRANE PROTEIN) (PHE-
 ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-
 NENT).//5.30E-11//142aa//30%//P32802
 C-HEMBA1001048//SARCALUMENIN PRECURSOR.//6.50E-18//154aa//33%//P13666
 45 C-HEMBA1001200
 C-HEMBA1001407
 C-HEMBA1001530//SLS1 PROTEIN PRECURSOR.//9.80E-10//273aa//27%//Q99158
 C-HEMBA1001547//Homo sapiens CGI-02 protein mRNA, complete cds.//0//2311bp//99%//AF132937
 C-HEMBA1001573
 50 C-HEMBA1001847//NEUROGENIC PROTEIN BIG BRAIN.//4.70E-06//258aa//24%//P23645
 C-HEMBA1001959//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN
 B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//7.30E-14//97aa//38%//P25210
 C-HEMBA1001978
 C-HEMBA1002039
 55 C-HEMBA1002041//Homo sapiens transmembrane protein TENB2 (TENB2) mRNA, complete cds.//0//1746bp//
 99%//AF179274
 C-HEMBA1002051//Homo sapiens Ets transcription factor ESE-2b mRNA, complete cds.//1.30E-95//454bp//99%//
 AF115403

- C-HEMBB1002120//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE
110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT) //4.90E-22//337aa//27%//P56558
C-HEMBB1002162//Homo sapiens genethonin 1 mRNA, complete cds.//8.30E-67//328bp//99%//AF062534
C-HEMBB1002228
5 C-HEMBB 1002245//PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR
(PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN) //0//879aa//89%//Q62786
C-HEMBB1002302
C-HEMBB1002427//FUCOSYLGLYCOPROTEIN ALPHA-N-ACETYLGLACTOSAMINYLTRANSFERASE (EC
2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3-AL-
10 PHA-GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANS-
FERASE) (NAGAT) //1.80E-70//221aa//50%//P16442
C-HEMBB1002465//ACYL-COA DEHYDROGENASE (EC 1.3.99.-) //2.30E-53//249aa//48%//P45857
C-HEMBB1002661//Homo sapiens cardiovascular helix-loop-helix factor 2 (CHF2) mRNA, complete cds.//0//
2174bp//99%//AF176422
15 C-HEMBB1002663
C-HEMBB1002693
C-MAMMA1000046
C-MAMMA1000102//APOLIPOPROTEIN L PRECURSOR (APO-L) //1.40E-21//221aa//35%//O14791
C-MAMMA1000106
20 C-MAMMA1000118
C-MAMMA1000141
C-MAMMA1000204//Homo sapiens dysferlin mRNA, complete cds.//0//2028bp//99%//AF075575
C-MAMMA1000226
C-MAMMA1000403//Homo sapiens CDK4-binding protein p34SEI1 (SEI1) mRNA, complete cds.//1.20E-255//
25 1165bp//99%//AF117959
C-MAMMA1000449
C-MAMMA1000457//Human NADH-cytochrome b5 reductase mRNA, 3' end.//9.50E-79//829bp//71%//M16462
C-MAMMA1000473//HYPOTHETICAL 35.6 KD PROTEIN IN SPC1-ILV3 INTERGENIC REGION.//5.10E-45//
299aa//34%//P47088
30 C-MAMMA1000496//MIC1 PROTEIN //3.00E-25//202aa//33%//P53258
C-MAMMA1000528
C-MAMMA1000591//POLYPEPTIDE N-ACETYLGLACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-
UDP ACETYLGLACTOSAMINYLTRANSFERASE) (UDP-GALNAC:POLYPEPTIDE, N- ACETYLGLACTOS-
AMINYLTRANSFERASE) (GALNAC-T1) //1.20E-115//515aa//49%//Q07537
35 C-MAMMA10006141//Homo sapiens pseudouridine synthase I (PUS1) mRNA, partial cds.//2.10E-302//1370bp//
99%//AF116238
C-MAMMA1000652
C-MAMMA1000681//PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1 //9.40E-82//311aa//52%//O08530
C-MAMMA1000706
40 C-MAMMA1000788//Bos taurus P14 (p14) mRNA, complete cds.//3.90E-85//502bp//89%//AF037349
C-MAMMA1000810
C-MAMMA1000814
C-MAMMA1000881//Homo sapiens protein kinase (SGK3) mRNA, complete cds.//0//1292bp//100%//AF169035
C-MAMMA1000986
45 C-MAMMA1000994//Homo sapiens ISLR(immunoglobulin superfamily containing leucine-rich repeat) mRNA,
complete cds, alternatively spliced transcript ISLR-2 //0//2211bp//99%//AB024536
C-MAMMA1001043//MRC OX-45 SURFACE ANTIGEN PRECURSOR (BCM1 SURFACE ANTIGEN) (BLAST-1)
(CD48) //2.90E-12//239aa//28%//P10252
C-MAMMA1001066
50 C-MAMMA1001094//Human potential transcriptional repressor NOT4Hp (NOT4H) mRNA, complete cds.//0//
1394bp//93%//UJ1267
C-MAMMA1001141
C-MAMMA1001150//PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU) //7.50E-304//587aa//68%//Q15139
C-MAMMA1001237//MONOCARBOXYLATE TRANSPORTER 2 (MCT 2) //7.70E-64//196aa//41%//P53988
55 C-MAMMA1001284
C-MAMMA1001310//HYPOTHETICAL 57.3 KD TRP-ASP REPEATS CONTAINING PROTEIN IN POM152-
REC114 INTERGENIC REGION //1.50E-67//441aa//37%//Q04225
C-MAMMA1001344

- C-MAMMA1001418//HYPOTHETICAL PROTEIN HI0519.//6.90E-27//181aa//38%//P44742
 C-MAMMA1001532//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//5.60E-126//319aa//56%//P51523
 C-MAMMA1001609//MYOSIN II HEAVY CHAIN, NON MUSCLE.//1.50E-26//204aa//38%//P05659
 5 C-MAMMA1001615//NEUROGENIC DIFFERENTIATION FACTOR 1.//3.80E-11//90aa//42%//Q13562
 C-MAMMA1001623
 C-MAMMA1001634
 C-MAMMA1001893
 C-MAMMA1001901
 10 C-MAMMA1001957
 C-MAMMA1001978//Cimex lectularius apyrase (APY) mRNA, complete cds.//6.70E-19//988bp//56%//AF085499
 C-MAMMA1002070//PLASMINOGEN (EC 3.4.21.7) (FRAGMENT).//1.10E-07//103aa//33%//Q01177
 C-MAMMA1002080//RAS-RELATED PROTEIN RAB-13.//1.80E-29//208aa//37%//P51153
 C-MAMMA1002087
 15 C-MAMMA1002091//Homo sapiens CD39L2 (CD39L2) mRNA, complete cds.//0//2564bp//99%//AF039916
 C-MAMMA1002095//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (P-TYPE CALCIUM ATPASE).//3.70E-222//867aa//52%//O43108
 C-MAMMA1002128//ABC1 PROTEIN HOMOLOG PRECURSOR.//2.50E-97//464aa//45%//Q92338
 C-MAMMA1002142//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PRO-
 20 TEIN KINASE 1).//9.80E-17//146aa//35%//P18160
 C-MAMMA1002165//Homo sapiens connective tissue growth factor related protein WISP-2 (WISP2) mRNA, complete cds.//4.80E-60//382bp//89%//AF100780
 C-MAMMA1002205//Homo sapiens mRNA; cDNA DKFZp586C091 (from clone DKFZp586C091).//2.00E-81//308bp//81%//AL050119
 25 C-MAMMA1002224
 C-MAMMA1002234//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//0//627aa//96%//Q00004
 C-MAMMA1002586//Homo sapiens alpha 1,2-mannosidase mRNA, complete cds.//0//2228bp//99%//AF148509
 C-MAMMA1002633
 C-MAMMA1003126//SARCALUMENIN PRECURSOR.//1.10E-51//388aa//32%//P13666
 30 C-NT2RM1000462//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//8.60E-14//104aa//40%//P15287
 C-NT2RM1000542//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//1.40E-103//566aa//43%//P48982
 C-NT2RM1000580//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//8.50E-75//301aa//39%//P43636
 35 C-NT2RM1000789//Homo sapiens mRNA for hTCF-4.//2.80E-221//757bp//99%//Y11306
 C-NT2RM1000855//Homo sapiens sec61 homolog mRNA, complete cds.//0//3541bp//99%//AF084458
 C-NT2RM1000858//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].//2.10E-98//1035bp//70%//S70011
 C-NT2RM1000899//MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.//1.10E-54//182aa//39%//P23500
 C-NT2RM2000241
 40 C-NT2RM2000306//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//4.50E-130//362aa//68%//P91917
 C-NT2RM2000410
 C-NT2RM2000423//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//1.80E-38//308aa//35%//P48982
 C-NT2RM2000497//CHL1 PROTEIN.//9.90E-24//296aa//29%//P22516
 45 C-NT2RM2000514//Homo sapiens F-box protein Fbx21 (FBX21) mRNA, complete cds.//4.40E-304//1374bp//99%//AF174601
 C-NT2RM2000565//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//4.40E-304//394aa//43%//Q09782
 C-NT2RM2000582//Homo sapiens mRNA for KIAA1053 protein, partial cds.//0//2666bp//99%//AB028976
 50 C-NT2RM2000589//Bos taurus myosin X, complete cds.//0//4376bp//84%//U55042
 C-NT2RM2000622//Mus musculus F-box protein FBL10 mRNA, partial cds.//3.00E-203//915bp//91%//AF176524
 C-NT2RM2000632//EXCISION REPAIR PROTEIN ERCC-6 (COCKAYNE SYNDROME PROTEIN CSB).//6.40E-62//183aa//47%//Q03468
 C-NT2RM2000773//Homo sapiens KNSL4 and MAZ genes for kinesin-like DNA binding protein and Myc-associated zinc finger protein, complete cds.//3.00E-289//1092bp//99%//AB017335
 55 C-NT2RM2001126//Homo sapiens mRNA for multi PDZ domain protein.//0//1600bp//99%//AJ001319
 C-NT2RM2001558//Homo sapiens protein kinase A binding protein AKAP110 mRNA, complete cds.//0//2398bp//99%//AF093408

- C-NT2RM2001626//FLIGHTLESS-I PROTEIN HOMOLOG.//4.30E-19//362aa//26%//P34268
 C-NT2RM2001643
 C-NT2RM2001738//SOF1 PROTEIN.//3.00E-110//325aa//47%//P33750
 C-NT2RM2001792//Homo sapiens angiotensin-related protein-2 mRNA, complete cds.//7.10E-149//995bp//86%//
 5 AF125175
 C-NT2RM2001818//SIALIDASE (EC 3.2.1.18) (NEURAMINIDASE) (NA) (MAJOR SURFACE ANTIGEN).//4.30E-
 11//488aa//26%//P23253
 C-NT2RM2001902//Homo sapiens mRNA for PAK4 protein.//5.40E-216//988bp//99%//AJ011855
 C-NT2RM2001939//Human G protein-coupled receptor GPR-NGA gene, complete cds.//0//1559bp//98%//U55312
 10 C-NT2RM2001941//MUSCARINIC ACETYLCHOLINE RECEPTOR M1.//7.40E-38//193aa//34%//P08482
 C-NT2RM4000100//Homo sapiens Leman coiled-coil protein (LCCP) mRNA, complete cds.//0//2678bp//99%//
 AF175966
 C-NT2RM4000115
 C-NT2RM4000198//BUTYROPHILIN PRECURSOR (BT).//5.10E-12//162aa//33%//Q13410
 15 C-NT2RM4000284//Human IgG Fc receptor hFcRn mRNA, complete cds.//1.30E-257//603bp//96%//U12255
 C-NT2RM4000295
 C-NT2RM4000326//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//9.00E-100//434aa//43%//
 P51523
 C-NT2RM4000417//SYNAPTOTAGMIN II.//2.70E-23//293aa//30%//P46097
 20 C-NT2RM4000444//ANTIGEN PEPTIDE TRANSPORTER 1 (APT1).//1.70E-112//493aa//44%//P36370
 C-NT2RM4000587
 C-NT2RM4000593//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME I.//3.90E-27//576aa//
 24%//Q10297
 C-NT2RM4000648//K-GLYPICAN PRECURSOR.//4.00E-193//531aa//66%//P51655
 25 C-NT2RM4000761//CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1).//2.50E-245//306aa//91%//
 P00395
 C-NT2RM4000965//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4 SUBUNIT).//9.00E-44//
 520aa//29%//O60100
 C-NT2RM4000997//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL).//1.80E-10//
 30 189aa//30%//P25234
 C-NT2RM4001321
 C-NT2RM4001325//CHONDROITIN 6-SULFOTRANSFERASE (EC 2.8.2.17) (C6ST).//2.90E-48//343aa//34%//
 Q92179
 C-NT2RM4001377//R.norvegicus LL5 mRNA.//8.50E-236//990bp//87%//X74226
 35 C-NT2RM4001735
 C-NT2RM4001768//Homo sapiens CGI-82 protein mRNA, complete cds.//0//1925bp//99%//AF151840
 C-NT2RM4001843//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//6.20E-33//263aa//38%//
 P48982
 C-NT2RM4002352//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds.//0//
 40 2184bp//99%//AB009462
 C-NT2RP1000002
 C-NT2RP1000050
 C-NT2RP1000181//Homo sapiens delta-6 fatty acid desaturase mRNA, complete cds.//3.30E-121//1394bp//69%//
 AF126799
 45 C-NT2RP1000239
 C-NT2RP1000261//ORM1 PROTEIN.//2.40E-17//137aa//35%//P53224
 C-NT2RP1000271//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//4.70E-199//547aa//
 66%//Q03923
 C-NT2RP1000300//Human transporter protein (g17) mRNA, complete cds.//3.80E-26//758bp//62%//U49082
 50 C-NT2RP1000325//H.sapiens gene for phosphate carrier.//0//439bp//98%//X77337
 C-NT2RP1000448
 C-NT2RP1000465//UBIQUITIN-LIKE PROTEIN SMT3.//5.10E-07//81aa//33%//P55857
 C-NT2RP1000468//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN
 B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//2.00E-13//97aa//38%//P25210
 55 C-NT2RP1000551//Homo sapiens putative interferon-related protein (SM15) mRNA, partial cds.//0//1761bp//
 99%//U09585
 C-NT2RP1000579//Human succinate dehydrogenase flavoprotein subunit (SDH) mRNA, complete cds.//0//
 1951bp//94%//L21936

C-NT2RP1000613//CARBONIC ANHYDRASE VI (EC 4.2.1.1) (SALIVARY) (CARBONATE DEHYDRATASE VI).//
 3.40E-52//304aa//40%//P08060
 C-NT2RP1000679
 C-NT2RP1000740
 5 C-NT2RP1000903
 C-NT2RP1000981//CELL SURFACE A33 ANTIGEN PRECURSOR.//3.60E-14//286aa//27%//Q99795
 C-NT2RP1001004//F-SPONDIN PRECURSOR.//9.20E-43//322aa//35%//P35446
 C-NT2RP1001020//SERINE/THREONINE-PROTEIN KINASE PAK-BETA (EC 2.7.1.-) (BETA-PAK) (P21-ACTI-
 VATED KINASE 3) (CDC42/RAC EFFECTOR KINASE PAK-B).//9.70E-22//227aa//31%//Q61036
 10 C-NT2RP1001031//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//3.40E-42//285aa//35%//Q00808
 C-NT2RP1001563//TESTIS-SPECIFIC PROTEIN TPX-1 PRECURSOR (AUTOANTIGEN 1) (25 KD ACROSOM-
 AL AUTOANTIGEN) (AA1).//9.70E-19//201aa//31%//Q60477
 C-NT2RP2000092//ZINC FINGER PROTEIN 136.//1.90E-117//419aa//54%//P52737
 C-NT2RP2000178//MITOCHONDRIAL ION PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//2.40E-192//
 15 778aa//48%//P93647
 C-NT2RP2000240
 C-NT2RP2000394//Gallus gallus p52 pro-apototic protein mRNA, complete cds.//1.60E-90//956bp//70%//
 AF029071
 C-NT2RP2000447//GOLGIN-95.//2.80E-33//99aa//66%//Q08379
 20 C-NT2RP2000479
 C-NT2RP2000514//Homo sapiens roundabout 2 (robo2) mRNA, partial cds.//3.00E-185//855bp//99%//AF040991
 C-NT2RP2000533//Homo sapiens cornichon protein mRNA, complete cds.//1.30E-290//1324bp//99%//AF070654
 C-NT2RP2000610//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN
 B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//1.50E-13//97aa//38%//P25210
 25 C-NT2RP2000616//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//
 4.10E-12//323aa//30%//P13983
 C-NT2RP2000649//Homo sapiens mRNA for Hs Ste24p, complete cds.//0//2847bp//99%//AB016068
 C-NT2RP2000663
 C-NT2RP2000694//Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.//0//2278bp//99%//AJ012159
 30 C-NT2RP2000712//ZINC FINGER PROTEIN 135.//3.70E-87//296aa//53%//P52742
 C-NT2RP2000739//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.50E-73//387aa//37%//
 P51522
 C-NT2RP2000818//Homo sapiens xenotropic and polytropic murine leukemia virus receptor (X3) mRNA, complete
 cds.//0//2724bp//99%//AF089744
 35 C-NT2RP2000903//Homo sapiens 5T4 oncofetal trophoblast glycoprotein gene.//0//2276bp//100%//AJ012159
 C-NT2RP2001200//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1539bp//100%//AB014576
 C-NT2RP2001223//MYOTUBULARIN-RELATED PROTEIN 3 (FRAGMENT).//3.30E-05//76aa//39%//Q13615
 C-NT2RP2001276//NPDC-1 PROTEIN PRECURSOR.//3.00E-133//331aa//77%//Q64322
 C-NT2RP2001388//TRNA-SPLICING ENDONUCLEASE SUBUNIT SEN2 (EC 3.1.27.9) (TRNA-INTRON ENDO-
 40 NUCLEASE).//5.90E-13//157aa//33%//P16658
 C-NT2RP2001469//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//1.30E-14//242aa//24%//Q00808
 C-NT2RP2001480//Homo sapiens thrombospondin 3 (THBS3) gene, complete cds.//0//2547bp//99%//L38969
 C-NT2RP2001495//Human transporter protein (g17) mRNA, complete cds.//2.20E-65//641bp//65%//U49082
 C-NT2RP2001514//PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).//1.20E-133//429aa//
 45 41%//P39986
 C-NT2RP2001529//Homo sapiens mRNA for ZIP-kinase, complete cds.//0//2079bp//99%//AB007144
 C-NT2RP2001538//Mus musculus mSin3A (sin3A) mRNA, complete cds.//7.60E-272//1480bp//84%//U22394
 C-NT2RP2001562//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//0//1899bp//98%//AF058922
 C-NT2RP2001662//HOMEODOMAIN PROTEIN AKR (AVIAN KNOTTED-RELATED PROTEIN).//1.80E-49//
 50 94aa//81%//Q90655
 C-NT2RP2001755//Rattus norvegicus f-spondin mRNA, complete cds.//0//2974bp//86%//M88469
 C-NT2RP2001769//SERINE/THREONINE-PROTEIN KINASE ORB6 (EC 2.7.1.-).//9.10E-47//185aa//44%//
 O13310
 C-NT2RP2001817//Homo sapiens sirtuin type 1 (SIRT1) mRNA, complete cds.//0//3092bp//99%//AF083106
 55 C-NT2RP2001878
 C-NT2RP2001903//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM- ACTIVATED NEU-
 TRAL PROTEINASE) (CANP) (MU/M-TYPE).//3.80E-58//475aa//34%//P00789
 C-NT2RP2001915

- C-NT2RP2001921
 C-NT2RP2001948//HST2 PROTEIN (HOMOLOGOUS TO SIR2 PROTEIN 2)//1.40E-08//191aa//27%//P53686
 C-NT2RP2001956//ORM1 PROTEIN//3.90E-19//137aa//37%//P53224
 C-NT2RP2002015
 5 C-NT2RP2002063//GNS1 PROTEIN//3.60E-18//231aa//33%//P25358
 C-NT2RP2002188//Rattus norvegicus neuroligin 3 mRNA, complete cds.//2.50E-226//1284bp//89%//U41663
 C-NT2RP2002232//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME I.//1.90E-93//420aa//43%//Q09782
 C-NT2RP2002304//Homo sapiens histone acetyltransferase MORF mRNA, complete cds.//0//2737bp//99%//AF113514
 10 C-NT2RP2002409
 C-NT2RP2002510
 C-NT2RP2002527//CYTOCHROME B5//1.30E-11//92aa//38%//P40312
 C-NT2RP2002533//Homo sapiens alpha 2 delta calcium channel subunit isoform I mRNA, complete cds.//0//2365bp//99%//AF042792
 15 C-NT2RP2002564//Human zinc-finger protein C2H2-150 mRNA, complete cds.//0//2237bp//99%//U38864
 C-NT2RP2002674//SOLUBLE EPOXIDE HYDROLASE (SEH) (EC 3.3.2.3) (EPOXIDE HYDRATASE) (CYTOSOLIC EPOXIDE HYDROLASE) (CEH)//5.50E-38//201aa//39%//P34913
 C-NT2RP2002721//REGULATORY PROTEIN UHPC//1.60E-23//153aa//30%//P27669
 20 C-NT2RP2002824//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT)//3.50E-63//404aa//33%//P32802
 C-NT2RP2002942//Homo sapiens mRNA for KIAA0806 protein, complete cds.//0//2090bp//99%//AB018349
 C-NT2RP2002974//HOMEODOMAIN PROTEIN SIXS (DM LOCUS-ASSOCIATED HOMEODOMAIN PROTEIN HOMOLOG) (FRAGMENT)//8.20E-241//555aa//84%//P70178
 25 C-NT2RP2002976//HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION//1.30E-20//99aa//47%//P38800
 C-NT2RP2003042//PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE) (FRAGMENT)//2.10E-109//385aa//52%//P53760
 30 C-NT2RP2003138//5'-TG-3' INTERACTING FACTOR (HOMEODOMAIN PROTEIN TGIF)//2.10E-08//104aa//46%//P70284
 C-NT2RP2003179//PUTATIVE SERINE/THREONINE-PROTEIN KINASE EMK (EC 2.7.1.-)//2.60E-67//256aa//49%//Q05512
 35 C-NT2RP2003210//Homo sapiens fatty acid transport protein (FATP) mRNA, complete cds.//9.80E-272//1265bp//98%//AF055899
 C-NT2RP2003302//Homo sapiens GIOT-4 mRNA for gonadotropin inducible transcription repressor-4, complete cds.//0//2891bp//99%//AB021644
 C-NT2RP2003369//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1)//5.90E-20//204aa//34%//Q15404
 40 C-NT2RP2003383//Homo sapiens mRNA for KIAA0458 protein, complete cds.//0//2565bp//99%//AB007927
 C-NT2RP2003390//Homo sapiens mRNA for SEC63 protein.//0//2629bp//99%//AJ011779
 C-NT2RP2003469//GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER)//1.10E-45//324aa//29%//P37021
 45 C-NT2RP2003545//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//5.40E-48//578bp//71%//AF024636
 C-NT2RP2003593
 C-NT2RP2003599
 C-NT2RP2003655//HYPOTHETICAL 26.3 KD PROTEIN IN OYE2-GND1 INTERGENIC//4.80E-15//93aa//47%//P38869
 50 C-NT2RP2003664//Homo sapiens mRNA for leptin receptor gene-related protein.//1.90E-237//1081bp//99%//Y12670
 C-NT2RP2003931
 C-NT2RP2003940//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6)//7.00E-111//401aa//43%//P28160
 55 C-NT2RP2003950//Homo sapiens clone 24778 unknown mRNA.//0//1545bp//99%//AF070572
 C-NT2RP2004069
 C-NT2RP2004108//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)//3.30E-171//474aa//62%//P16415
 C-NT2RP2004141

C-NT2RP2004179
 C-NT2RP2004205//BUTYROPHILIN PRECURSOR (BT)//1.60E-21//276aa//32%//Q62556
 C-NT2RP2004447
 C-NT2RP2004495//Human transporter protein (g17) mRNA, complete cds.//9.80E-64//642bp//64%//L149082
 5 C-NT2RP2004524
 C-NT2RP2004556
 C-NT2RP2004606//Human fibroblast collagenase inhibitor mRNA, complete cds.//2.10E-166//768bp//99%//M12670
 C-NT2RP2004648//Mouse beta-galactosidase (BGAL) gene, complete cds.//1.20E-33//1136bp//59%//M57734
 10 C-NT2RP2004670//Rattus norvegicus vesicle-associate calmodulin-binding protein mRNA, complete cds.//0//1250bp//86%//L22557
 C-NT2RP2004794//HYPOTHETICAL 24.5 KD PROTEIN IN SAP185-BCK1 INTERGENIC REGION.//2.70E-09//203aa//26%//P40857
 C-NT2RP2004837
 15 C-NT2RP2004847//ZINC FINGER PROTEIN 135.//8.00E-35//193aa//40%//P52742
 C-NT2RP2005027//GLUCOSE TRANSPORTER TYPE 3, BRAIN.//6.20E-67//130aa//100%//P11169
 C-NT2RP2005069//Rat vacuolar protein sorting homolog vps33b mRNA, complete cds.//0//1792bp//87%//U35245
 C-NT2RP2005163
 20 C-NT2RP2005181//Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds.//5.30E-315//2126bp//81%//U70859
 C-NT2RP2005247//ZINC-FINGER PROTEIN RFP (RET FINGER PROTEIN).//5.00E-53//296aa//37%//Q62158
 C-NT2RP2005378//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1.8 PRECURSOR (GRP 1.8).//6.30E-28//183aa//47%//P10496
 25 C-NT2RP2005391//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Sp1.//0//1544bp//99%//AJ242978
 C-NT2RP2005425//Homo sapiens mRNA for AKAP450 protein.//0//4341bp//99%//AJ131693
 C-NT2RP2005463//PROTEIN PTM1 PRECURSOR.//7.40E-15//284aa//28%//P32857
 C-NT2RP2005514
 30 C-NT2RP2005535//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (HTF1).//1.90E-172//489aa//62%//Q03923
 C-NT2RP2005541//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).//4.70E-24//78aa//51%//P15586
 C-NT2RP2005597//Homo sapiens protein O-mannosyl-transferase 1 (POMT1) mRNA, complete cds.//0//1821bp//97%//AF095136
 35 C-NT2RP2005632
 C-NT2RP2005666
 C-NT2RP2005774//Homo sapiens GIOT-4 mRNA for gonadotropin inducible transcription repressor-4, complete cds.//6.90E-224//1461bp//72%//AB021644
 40 C-NT2RP2005878//PUTATIVE STEROID DEHYDROGENASE KIK-I (EC 1.1.1.-).//3.60E-55//238aa//50%//O57314
 C-NT2RP2005883//DOPAMINE-BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA-HYDROXYLASE) (DBH).//6.70E-72//512aa//34%//P15101
 C-NT2RP2005887
 45 C-NT2RP2005941//Human paired box gene (PAX6) homologue, complete cds.//1.40E-308//1396bp//99%//M93650
 C-NT2RP2005994//HYPOTHETICAL 51.5 KD PROTEIN D2024.3 IN CHROMOSOME IV.//3.50E-35//144aa//47%//P49191
 C-NT2RP2006004//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//3.00E-26//227aa//36%//Q06828
 50 C-NT2RP2006042//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.40E-15//501aa//25%//P08640
 C-NT2RP2006092//Homo sapiens mRNA for Fe65L2, complete cds.//0//1156bp//99%//AB018247
 C-NT2RP2006099
 55 C-NT2RP2006134
 C-NT2RP2006269//DOLICHYL-PHOSPHATE-MANNOSE--PROTEIN MANNOSYLTRANSFERASE 2 (EC 2.4.1.109).//2.30E-78//679aa//32%//P31382
 C-NT2RP2006512//GNS1 PROTEIN.//2.00E-21//290aa//29%//P25358

- C-NT2RP2006580//Homo sapiens transitional epithelia response protein (TERE1) mRNA, complete cds.//0//1483bp//99%//AF117064
- C-NT2RP3000011//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//4.00E-14//320aa//24%//Q00808
- 5 C-NT2RP3000022//Rat heart mRNA serine/threonine protein kinase, complete cds.//4.80E-203//1496bp//78%//D26178
- C-NT2RP3000059//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NONERYTHROID) (FRAGMENT).//3.70E-12//133aa//32%//Q01485
- C-NT2RP3000063//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//5.00E-29//596aa//30%//P19246
- 10 C-NT2RP3000125//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).//6.30E-08//70aa//41%//P29375
- C-NT2RP3000148//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//4.10E-106//350aa//47%//P51523
- C-NT2RP3000169//Homo sapiens MRS1 mRNA, complete cds.//0//1519bp//97%//AF093239
- 15 C-NT2RP3000171//Mus musculus partial mRNA for B-IND1 protein (B-ind1 gene).//4.40E-99//571bp//89%//Z97207
- C-NT2RP3000172//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KINASE I).//1.30E-80//359aa//44%//Q14012
- C-NT2RP3000201//Homo sapiens HPK/GCK-like kinase HGK mRNA, complete cds.//1.30E-270//1231bp//99%//AF096300
- 20 C-NT2RP3000232//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.40E-130//693aa//41%//Q99676
- C-NT2RP3000304//Homo sapiens LDL receptor-related protein 6 (LRP6) mRNA, complete cds.//0//2895bp//99%//AF074264
- C-NT2RP3000378//PAIRED AMPHIPATHIC HELIX PROTEIN.//4.20E-39//186aa//36%//P22579
- C-NT2RP3000427
- 25 C-NT2RP3000436//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.20E-27//90aa//42%//P38660
- C-NT2RP3000444
- C-NT2RP3000460//Canis familiaris sec61 homologue mRNA, complete cds.//1.80E-198//643bp//89%//M96629
- C-NT2RP3000481//Homo sapiens RanBP7/importin 7 mRNA, complete cds.//0//2623bp//100%//AF098799
- 30 C-NT2RP3000616//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//5.20E-26//227aa//36%//Q06828
- C-NT2RP3000645
- C-NT2RP3000652//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.90E-153//441aa//62%//P28160
- C-NT2RP3000676//PUTATIVE MITOCHONDRIAL CARRIER YMR166C.//2.10E-15//220aa//27%//Q03829
- 35 C-NT2RP3000677//DNA BINDING PROTEIN RFX2.//3.60E-56//233aa//41%//P48378
- C-NT2RP3000721//HYPOTHETICAL 149.7 KD PROTEIN IN IRE1-KSP1 INTERGENIC REGION.//1.10E-22//171aa//36%//P38800
- C-NT2RP3000789//Homo sapiens IGF-II mRNA-binding protein 1 (IMP-1) mRNA, complete cds.//0//1458bp//100%//AF117106
- 40 C-NT2RP3000818
- C-NT2RP3000820//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//1.90E-30//269aa//33%//P49695
- C-NT2RP3000838//TRICHOHYALIN.//9.80E-11//491aa//26%//Q07283
- C-NT2RP3000871
- 45 C-NT2RP3000907//PROBABLE CALCIUM-TRANSPORTING ATPASE 6 (EC 3.6.1.38).//2.20E-134//296aa//42%//P39986
- C-NT2RP3000921//TUMOR SUPPRESSOR PROTEIN DCC PRECURSOR (COLORECTAL CANCER SUPPRESSOR).//4.00E-21//316aa//29%//P43146
- C-NT2RP3001012//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//2906bp//98%//AB020636
- 50 C-NT2RP3001044
- C-NT2RP3001061//Homo sapiens mRNA for KIAA0853 protein, partial cds.//0//3591bp//99%//AB020660
- C-NT2RP3001159//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2558bp//99%//AL050118
- 55 C-NT2RP3001170//Mus musculus activity-dependent neuroprotective protein (Adnp) mRNA, complete cds.//4.80E-240//850bp//88%//AF068198
- C-NT2RP3001195//GALACTOSE-PROTON SYMPORT (GALACTOSE TRANSPORTER).//4.70E-48//339aa//29%//P37021
- C-NT2RP3001240//Canis familiaris sec61 homologue mRNA, complete cds.//1.20E-301//1141bp//89%//M96629

- C-NT2RP3001271//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//
2.60E-09//34aa//22%//P52178
- C-NT2RP3001322//PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (EC 3.6.1.38) (ENDOPLASMIC RETIC-
ULUM CA2+-ATPASE).//1.70E-21//220aa//30%//P39524
- 5 C-NT2RP3001388//SYNAPTOTAGMIN IV.//2.00E-118//430aa//54%//P50232
- C-NT2RP3001542//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-
TEIN).//4.70E-11//132aa//37%//Q13829
- C-NT2RP3001560//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//
0//2468bp//99%//AF037339
- 10 C-NT2RP3001592//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC
2.1.1.32).//1.30E-18//279aa//27%//P15565
- C-NT2RP3001650//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).//2.20E-22//
107aa//42%//P98063
- C-NT2RP3001685//PRPE PROTEIN.//1.00E-68//382aa//41%//P77495
- 15 C-NT2RP3001738//CYTOCHROME B5.//1.30E-11//133aa//33%//P00169
- C-NT2RP3001754
- C-NT2RP3001858
- C-NT2RP3001976//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//8.90E-143//379aa//55%//
P51523
- 20 C-NT2RP3002015//Homo sapiens CGI-71 protein mRNA, complete cds.//0//1991bp//99%//AF151829
- C-NT2RP3002160//HISTO-BLOOD GROUP ABO SYSTEM TRANSFERASE (NAGAT) [INCLUDES: GLYCO-
PROTEIN-FUCOSYLGALACTOSIDE ALPHA-N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.40)
(FUCOSYLGLYCOPROTEIN ALPHA-N-ACETYLGALACTOSAMINYLTRANSFERASE) (HISTO-BLOOD GROUP
A TRANSFERASE) (A TRANSFERASE); GLYCOPROTEIN-FUCOSYLGALACTOSIDE ALPHA- GALACTOSYL-
TRANSFERASE (EC 2.4.1.37) (FUCOSYLGLYCOPROTEIN 3-ALPHA- GALACTOSYLTRANSFERASE) (HISTO-
25 BLOOD GROUP B TRANSFERASE) (B TRANSFERASE)].//3.50E-72//231aa//49%//P16442
- C-NT2RP3002281//Homo sapiens mRNA for KIAA0765 protein, partial cds.//0//2286bp//99%//AB018308
- C-NT2RP3002286//Homo sapiens candidate tumor suppressor protein DICE1 mRNA, complete cds.//0//2719bp//
99%//AF097645
- 30 C-NT2RP3002311//BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE).//9.80E-103//547aa//
43%//P48982
- C-NT2RP3002324
- C-NT2RP3002342//Human transporter protein (g17) mRNA, complete cds.//1.70E-65//641bp//65%//U49082
- C-NT2RP3002353
- 35 C-NT2RP3002409//Homo sapiens mRNA for KIAA0719 protein, complete cds.//0//2404bp//99%//AB018262
- C-NT2RP3002411//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2374bp//99%//
AF078850
- C-NT2RP3002448
- C-NT2RP3002571//Bos taurus mRNA for lyncein.//7.30E-169//1115bp//84%//Y17923
- 40 C-NT2RP3002664
- C-NT2RP3002721//CITRATE SYNTHASE, MITOCHONDRIAL PRECURSOR (EC 4.1.3.7).//5.80E-249//466aa//
98%//O75390
- C-NT2RP3002737//Homo sapiens voltage-gated potassium channel KCNQ4 (KCNQ4) mRNA, complete cds.//0//
1552bp//99%//AF105202
- 45 C-NT2RP3002738//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds.//2.20E-47//763bp//
65%//L43821
- C-NT2RP3002790
- C-NT2RP3002836//Homo sapiens mRNA for KIAA0463 protein, partial cds.//0//1617bp//99%//AB007932
- C-NT2RP3002887
- 50 C-NT2RP3002900//Homo sapiens CGI-109 protein mRNA, complete cds.//8.70E-298//1321bp//92%//AF151867
- C-NT2RP3002958//TRANS-GOLGI NETWORK INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR.//
8.00E-08//197aa//26%//P19814
- C-NT2RP3002983
- C-NT2RP3003000//Homo sapiens T-type calcium channel alpha-1 subunit mRNA, complete cds.//0//3160bp//
96%//AF051946
- 55 C-NT2RP3003076
- C-NT2RP3003354//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 3.//5.10E-55//208aa//51%//
O35609

- C-NT2RP3003448
 C-NT2RP3003469
 C-NT2RP3003473//Homo sapiens CGI-55 protein mRNA, complete cds.//5.50E-275//1309bp//98%//AF151813
 C-NT2RP3003527//Homo sapiens mRNA for protein kinase Dyrk1B.//0//2483bp//99%//Y17999
 5 C-NT2RP3003532//OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR (FRAGMENT).//4.40E-139//263aa//99%//P41217
 C-NT2RP3003535//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P110 SUBUNIT).//8.80E-18//368aa//25%//P56558
 C-NT2RP3003559
 10 C-NT2RP3003614
 C-NT2RP3003729//HYPOTHETICAL 42.1 KD PROTEIN IN SNZ1-YPK2 INTERGENIC REGION.//5.80E-17//204aa//30%//Q03151
 C-NT2RP3003849//PROTEIN KINASE C, BRAIN ISOZYME (EC 2.7.1.-) (PKC) (DPKC53E(BR)). PKC1.//1.20E-13//126aa//34%//P05130
 15 C-NT2RP3003874//Homo sapiens incomplete cDNA for a mutated allele of a myosin class I, myh-1c.//0//2160bp//98%//AJ001381
 C-NT2RP3003963
 C-NT2RP3004000
 C-NT2RP3004025
 20 C-NT2RP3004067//Homo sapiens mRNA for NESCA, complete cds.//0//1962bp//99%//AB026894
 C-NT2RP3004075
 C-NT2RP3004083
 C-NT2RP3004090//GOLIATH PROTEIN (G1 PROTEIN).//9.00E-33//179aa//47%//Q06003
 C-NT2RP3004119//PEREGRIN (BR140 PROTEIN).//7.30E-39//227aa//43%//P55201
 25 C-NT2RP3004130//CELL SURFACE ANTIGEN 114/A10 PRECURSOR.//8.10E-06//71aa//42%//P19467
 C-NT2RP3004133//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//2.50E-48//198aa//37%//P43636
 C-NT2RP3004202
 C-NT2RP3004294//Xenopus laevis ER1 mRNA, complete cds.//1.20E-71//335bp//79%//AF015454
 C-NT2RP3004309//Homo sapiens mRNA; cDNA DKFZp586C201 (from clone DKFZp586C201).//0//2584bp//99%//AL050118
 30 C-NT2RP3004321
 C-NT2RP3004345//N2,N2-DIMETHYLGUANOSINE TRNA METHYLTRANSFERASE PRECURSOR (EC 2.1.1.32).//3.90E-18//279aa//27%//P15565
 C-NT2RP3004355
 35 C-NT2RP3004374
 C-NT2RP3004406//HYPOTHETICAL 37.4 KD PROTEIN IN IRR1-TIM44 INTERGENIC REGION.//3.20E-15//165aa//33%//P40544
 C-NT2RP3004481//BUTYROPHILIN PRECURSOR (BT).//8.50E-22//276aa//32%//Q62556
 C-NT2RP3004552//COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).//8.50E-24//263aa//33%//P17927
 40 C-NT2RP3004557//Human Ki nuclear autoantigen mRNA, complete cds.//0//2181bp//96%//U11292
 C-NT2RP3004625//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//1339bp//99%//AF082516
 C-NT2RP3004640//Bos taurus tuftelin mRNA, complete cds.//0//1204bp//88%//AF105228
 45 C-NT2RP3004647//PUTATIVE MITOCHONDRIAL CARRIER YMR166C.//2.00E-15//220aa//27%//Q03829
 C-NT2RP4000108//Human gene for neurofilament subunit NF-L.//0//1998bp//99%//X05608
 C-NT2RP4000634//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//0//1501bp//98%//AF111105
 C-NT2RP4000962//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//2.60E-18//225aa//32%//P08458
 50 C-NT2RP4001001//Homo sapiens clone 24856 mRNA sequence, complete cds.//3.90E-301//1374bp//99%//AF131856
 C-NT2RP4001009//Homo sapiens mRNA for farnesylated-proteins converting enzyme 1.//0//2965bp//99%//Y13834
 C-NT2RP4001467//Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).//0//2140bp//99%//X55740
 55 C-NT2RP4001877//Homo sapiens ribonucleoprotein RBM8 (RBM8) mRNA, complete cds.//0//2770bp//99%//AF127761
 C-NT2RP4001879
 C-NT2RP4002187//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2373bp//99%//

AF078850
 C-NT2RP4002451
 C-NT2RP4002715
 C-NT2RP4002750//Mus musculus cationic amino acid transporter (CAT3) mRNA, complete cds.//1.00E-310//
 5 2084bp//81%//U70859
 C-OVARC1000003//Homo sapiens sodium dependent phosphate transporter isoform NaPi-3b mRNA, complete
 cds.//4.30E-220//1158bp//94%//AF111856
 C-OVARC1000090
 C-OVARC1000105//UBIQUITIN-CONJUGATING ENZYME E2-28.4 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN
 10 LIGASE) (UBIQUITIN CARRIER PROTEIN) //4.20E-47//171aa//56%//P33296
 C-OVARC1000137
 C-OVARC1000208//Human calcium-dependent group X phospholipase A2 mRNA, complete cds//1.50E-61//
 365bp//90%//U95301
 C-OVARC1000255//H.sapiens syk mRNA for protein-tyrosine kinase.//0//1525bp//97%//Z29630
 15 C-OVARC1000275//DESMOPLAKIN I AND II (DPI AND DPII) (FRAGMENT) //9.90E-16//352aa//23%//P15924
 C-OVARC1000298
 C-OVARC1000307//HYPOTHETICAL 29.7 KD PROTEIN CY339.02.//3.00E-19//194aa//35%//Q50658
 C-OVARC1000313//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1) //3.00E-24//353aa//
 20 27%//Q12730
 C-OVARC1000331//GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCT-
 ASE) //9.40E-44//106aa//59%//P36959
 C-OVARC1000410//Homo sapiens angiopoietin Y1 mRNA, complete cds.//2.10E-63//744bp//69%//AF107253
 C-OVARC1000439//HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III.//1.40E-
 33//143aa//53%//P34280
 25 C-OVARC1000467
 C-OVARC1000529//PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-) //1.40E-23//
 165aa//39%//P34244
 C-OVARC1000553//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (THYMOCYTE-ACTIVATING MOLE-
 CULE) (THAM) //1.30E-23//169aa//40%//P28843
 30 C-OVARC1000775
 C-OVARC1000811//PLASMINOGEN (EC 3.4.21.7) (FRAGMENT) //6.40E-13//115aa//34%//Q01177
 C-OVARC1000853
 C-OVARC1000873//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLU-
 COSAMINE-6-SULFATASE) //1.00E-09//83aa//40%//P50426
 35 C-OVARC1000916//H.sapiens PISSLRE mRNA.//7.30E-280//1117bp//95%//X78342
 C-OVARC1000956//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG
 PROTEIN) //2.20E-09//250aa//28%//P17437
 C-OVARC1000995
 C-OVARC1001030//Homo sapiens mRNA for KIAA0886 protein, complete cds.//0//907bp//99%//AB020693
 40 C-OVARC1001049//TRANSCRIPTION FACTOR HES-1 (C-HAIRY1) //7.50E-14//96aa//36%//O57337
 C-OVARC1001086//Homo sapiens cyclin T2a mRNA, complete cds.//0//1593bp//98%//AF048731
 C-OVARC1001132//GC-RICH SEQUENCE DNA-BINDING FACTOR (GCF) (TRANSCRIPTION FACTOR 9) (TCF-
 9) //2.30E-44//268aa//36%//P16383
 C-OVARC1001163//HYPOTHETICAL 49.3 KD PROTEIN C30D11.06C IN CHROMOSOME I.//2.30E-20//152aa//
 45 30%//Q09906
 C-OVARC1001222
 C-OVARC1001260
 C-OVARC1001336//Homo sapiens sodium dependent phosphate transporter isoform NaPi-3b mRNA, complete
 cds.//0//1435bp//99%//AF111856
 50 C-OVARC1001338//AUTOPHAGY SERINE/THREONINE-PROTEIN KINASE APG1 (EC 2.7.1.-) //8.80E-30//
 125aa//40%//P53104
 C-OVARC1001569//PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W (EC 2.7.1.-) //1.50E-22//
 164aa//39%//P34244
 C-OVARC1001570//Homo sapiens beta-site APP cleaving enzyme (BACE) mRNA, complete cds.//0//1792bp//
 55 100%//AF190725
 C-OVARC1001596//Homo sapiens Arf-like 2 binding protein BART1 mRNA, complete cds.//0//1766bp//99%//
 AF126062
 C-OVARC1001607//Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.//0//

- 1836bp//96%//U15128
 C-OVARC1001725//Homo sapiens patched related protein TRC8 (TRC8) gene, exon 1 and partial cds.//0//
 1624bp//99%//AF064800
 C-OVARC1001727
- 5 C-OVARC1001807//Human TR3 orphan receptor mRNA, complete cds.//1.10E-243//1145bp//98%//L13740
 C-OVARC1001833//CIS-GOLGI MATRIX PROTEIN GM130.//6.60E-136//363aa//76%//Q62839
 C-OVARC1001952//TRICHOHYALIN.//3.30E-16//487aa//27%//Q07283
 C-OVARC1001991//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSHIID).//8.30E-06//114aa//
 35%//Q01956
- 10 C-OVARC1002058//Human 18S rRNA gene, complete.//1.50E-164//921bp//91%//M10098
 C-OVARC1002178
 C-PLACE1000033//VON WILLEBRAND FACTOR PRECURSOR.//3.80E-17//190aa//28%//Q28295
 C-PLACE1000231//Rattus norvegicus WAP four-disulfide core domain protein (ps20) mRNA, complete cds.//
 2.70E-101//947bp//74%//AF037272
- 15 C-PLACE1000258//ZINC FINGER. PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.70E-55//431aa//
 35%//Q05481
 C-PLACE1000442//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//1.00E-88//213aa//67%//P16415
 C-PLACE1000560
 C-PLACE1000740//Mus musculus (Notch2) mRNA, complete cds.//5.60E-122//893bp//81%//M93661
- 20 C-PLACE1000907//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.30E-204//396aa//85%//
 P51522
 C-PLACE1000912
 C-PLACE1000914//Homo sapiens PB39 mRNA, complete cds.//7.50E-88//500bp//69%//AF045584
 C-PLACE1000927//HYPOTHETICAL 20.9 KD PROTEIN B0563.3 IN CHROMOSOME X.//6.30E-21//123aa//
 37%//Q11079
- 25 C-PLACE1000986//Homo sapiens mRNA; cDNA DKFZp586C1817 (from clone DKFZp586C1817).//0//2055bp//
 99%//AL117450
 C-PLACE1001016//SODIUM CHANNEL PROTEIN PARA (PARALYTIC PROTEIN).//6.80E-12//133aa//28%//
 P35500
- 30 C-PLACE1001100//Homo sapiens nephrin (NPHS1) mRNA, complete cds.//3.10E-46//323bp//84%//AF035835
 C-PLACE1001114//HYPOTHETICAL BHLF1 PROTEIN.//9.20E-06//389aa//31%//P03181
 C-PLACE1001123//INTESTINAL MEMBRANE A4 PROTEIN (DIFFERENTIATION-DEPENDENT PROTEIN A4).//
 5.00E-08//95aa//31%//Q04941
- 35 C-PLACE1001183
 C-PLACE1001229
 C-PLACE1001231//Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA, complete
 cds.//2.20E-137//918bp//80%//AF026554
 C-PLACE1001340//MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRI-
 AL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER)
- 40 (TRANSLOCASE OF OUTER MEMBRANE TOM70).//1.20E-23//231aa//31%//P23231
 C-PLACE1001401//HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCER1) (IGE
 FC RECEPTOR, BETA-SUBUNIT).//3.70E-18//148aa//39%//P13386
 C-PLACE1001407
 C-PLACE1001464//Human placental cDNA coding for 5'nucleotidase (EC 3.1.3.5).//0//2756bp//99%//X55740
- 45 C-PLACE1001500//Homo sapiens RecQ5 mRNA for DNA helicase, complete cds.//2.30E-271//1230bp//99%//
 AB006533
 C-PLACE1001516//240 KD PROTEIN OF ROD PHOTORECEPTOR CNG-CHANNEL [CONTAINS: GLUTAMIC
 ACID-RICH PROTEIN (GARP); CYCLIC-NUCLEOTIDE-GATED CATION CHANNEL 4 (CNG CHANNEL 4) (CNG-
 4) (CYCLIC NUCLEOTIDE-GATED CATION CHANNEL MODULATORY SUBUNIT)].//2.30E-08//274aa//28%//
 Q28181
- 50 C-PLACE1001536
 C-PLACE1001564//H.sapiens mRNA for HE6 Tm7 receptor.//5.10E-36//499bp//70%//X81892
 C-PLACE1001655//Homo sapiens Shab-related delayed-rectifier K+ channel alpha subunit (KCNS3) mRNA, com-
 plete cds.//0//1708bp//99%//AF043472
- 55 C-PLACE1001788
 C-PLACE1001795//HYPOTHETICAL 30.6 KD PROTEIN IN SCP160-SMC3 INTERGENIC REGION PRECUR-
 SOR.//3.40E-20//159aa//40%//P47032
 C-PLACE1001836//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: OUTER MEM-

- BRANE PROTEIN GP70; TRANSMEMBRANE PROTEIN P20E].//5.00E-27//134aa//47%/P10269
 C-PLACE1001918//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHE-
 ROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPO-
 NENT).//2.30E-53//339aa//33%/P32802
- 5 C-PLACE1001949//PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).//3.00E-75//315aa//44%/Q12697
 C-PLACE1002080//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//0//1588bp//99%/AF039691
 C-PLACE1002095
 C-PLACE1002153//Homo sapiens TACC2 protein (TACC2) mRNA, partial cds.//0//1202bp//99%/AF095791
- 10 C-PLACE1002329//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//6.50E-105//213aa//45%/Q08509
 C-PLACE1002355//COMPLEMENT C4 PRECURSOR [CONTAINS: C4A ANAPHYLATOXIN].//4.20E-12//131aa//40%/P01029
 C-PLACE1002374//Human mRNA for pro-cathepsin L (major excreted protein MEP).//1.30E-313//1363bp//97%/X12451
- 15 C-PLACE1002518//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//2.50E-14//396bp//64%/AF064801
 C-PLACE1002547//MITOCHONDRIAL PRECURSOR PROTEINS IMPORT RECEPTOR (72 KD MITOCHONDRIAL OUTER MEMBRANE PROTEIN) (MITOCHONDRIAL IMPORT RECEPTOR FOR THE ADP/ATP CARRIER) (TRANSLOCASE OF OUTER MEMBRANE TOM70).//2.30E-28//277aa//31%/P23231
- 20 C-PLACE1002726//Oryctolagus cuniculus mRNA for epithelial calcium channel (ECaC).//2.80E-202//926bp//82%/AJ133128
 C-PLACE1002905//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASSOCIATED DIAZEPAM BINDING INHIBITOR) (MA-DBI).//2.40E-37//188aa//40%/P07106
- 25 C-PLACE1002911//POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR.//4.50E-39//345aa//32%/P32507
 C-PLACE1002967//HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR BETA-SUBUNIT (FCERI) (IGE FC RECEPTOR, BETA-SUBUNIT).//4.60E-08//156aa//30%/Q01362
 C-PLACE1003135//SPORULATION-SPECIFIC PROTEIN 1 (EC 2.7.1.-).//1.30E-47//210aa//49%/P08458
 C-PLACE1003163//Homo sapiens DBI-related protein mRNA, complete cds.//1.00E-294//1344bp//99%/AF069301
- 30 C-PLACE1003407//Homo sapiens putative transmembrane protein (CLN5) mRNA, complete cds.//0//1965bp//99%/AF068227
 C-PLACE1003428//Homo sapiens mRNA for VNN1 protein.//1.80E-142//676bp//72%/AJ132099
 C-PLACE1003438
 C-PLACE1003460
- 35 C-PLACE1003529//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//1.30E-09//281aa//22%/P11414
 C-PLACE1003573//T-CELL SURFACE GLYCOPROTEIN YE1/48 (T LYMPHOCYTE ANTIGEN A1) (LY49-A ANTIGEN).//3.70E-16//226aa//26%/P20937
- 40 C-PLACE1003598//TRP-ASP REPEATS CONTAINING PROTEIN RBA-1.//1.80E-07//161aa//27%/P90917
 C-PLACE1003644
 C-PLACE1003737//TOLL PROTEIN PRECURSOR.//5.40E-07//203aa//27%/P08953
 C-PLACE1003772//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//2.40E-12//124aa//38%/P13983
- 45 C-PLACE1003839//Homo sapiens putative G protein-coupled receptor (RAIG1) mRNA, complete cds.//8.10E-18//771bp//58%/AF095448
 C-PLACE1003845//PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE).//3.40E-37//302aa//30%/Q57664
 C-PLACE1003852//Homo sapiens mRNA for KIAA0758 protein, partial cds.//0//1667bp//99%/AB018301
- 50 C-PLACE1004028
 C-PLACE1004078//Bovine mRNA for adseverin, complete cds.//0//2218bp//89%/D26549
 C-PLACE1004166//CREB-BINDING PROTEIN.//1.80E-12//147aa//35%/P45481
 C-PLACE1004168//GENERAL NEGATIVE REGULATOR OF TRANSCRIPTION SUBUNIT 1.//9.10E-62//485aa//32%/P25655
- 55 C-PLACE1004199
 C-PLACE1004279//HYPOTHETICAL 59.1 KD PROTEIN, ZK637.1 IN CHROMOSOME III.//1.40E-08//166aa//30%/P30638
 C-PLACE1004282//MONO- AND DIACYLGLYCEROL LIPASE PRECURSOR (EC 3.1.1.-) (MDGL).//2.10E-11//

- 189aa//30%//P25234
 C-PLACE1004305//RAS-RELATED PROTEIN RAC1.//9.60E-29//197aa//41%//P40792
 C-PLACE1004441//Human G protein-coupled receptor (GPR1) gene, complete cds.//0//1880bp//98%//U13666
 C-PLACE1004450//AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (LEUKEMIA AN-
 5 TIGEN CD13) //1.30E-91//562aa//35%//P15541
 C-PLACE1004482//Rattus norvegicus hematopoietic lineage switch 2 related protein (Hls2-rp) mRNA, complete
 cds.//1.90E-246//1643bp//83%//AF097723
 C-PLACE1004492//VERPROLIN//3.30E-07//149aa//29%//P37370
 C-PLACE1004519
 10 C-PLACE1004520//Human pregnancy-specific beta-glycoprotein d mRNA, complete cds.//9.10E-279//882bp//
 88%//M20881
 C-PLACE1004630//Homo sapiens ten integrin EGF-like repeat domains protein precursor (ITGBL1) mRNA, com-
 plete cds.//1.00E-138//643bp//99%//AF072752
 C-PLACE1004637
 15 C-PLACE1004648//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA- GLUCOSI-
 DASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) //1.40E-18//395aa//25%//P08640
 C-PLACE1004816//Homo sapiens mRNA for Hakata antigen, complete cds.//1.00E-166//856bp//94%//D88587
 C-PLACE1004887//GOLIATH PROTEIN (G1 PROTENN) //4.80E-33//179aa//47%//Q06003
 C-PLACE1005003//PROSTASIN PRECURSOR (EC 3.4.21.-) //2.20E-52//269aa//41%//Q16651
 20 C-PLACE1005005//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2G2) mRNA, complete cds.//4.10E-261//
 1209bp//98%//AF032456
 C-PLACE1005031//CHLORINE CHANNEL PROTEIN P64.//8.00E-92//205aa//87%//P35526
 C-PLACE1005239//Homo sapiens mRNA for HIRIP3 protein (clone pH4-31, PH4-17) //1.80E-235//1010bp//84%//
 AJ2233511
 25 C-PLACE1005250//Homo sapiens D-type cyclin-interacting protein 1 (DIP1) mRNA, complete cds.//0//1046bp//
 96%//AF082569
 C-PLACE1005383//Homo sapiens UP50 mRNA, complete cds.//0//2019bp//99%//AF093118
 C-PLACE1005410//Canis familiaris sec61 homologue mRNA, complete cds.//2.40E-204//673bp//89%//M96629
 C-PLACE1005426//Human pregnancy-specific beta 1-glycoprotein 4 (PSG4) clone FL-64 mRNA, complete cds.//
 0//1629bp//95%//U18469
 30 C-PLACE1005519//Homo sapiens STE20-like kinase 3 (mst-3) mRNA, complete cds.//4.60E-108//1070bp//73%//
 AF024636
 C-PLACE1005539//ACTIN POLYMERIZATION INHIBITOR (HEAT SHOCK 25 KD PROTEIN) (25-KD IAP) //3.10E-08//84aa//34%//Q00649
 35 C-PLACE1005544//Mus musculus junctional adhesion molecule (Jam) mRNA, complete cds.//2.00E-159//
 1237bp//76%//U89915
 C-PLACE1005569//Homo sapiens mRNA for Z39lg protein.//0//1768bp//99%//AJ132502
 C-PLACE1005601
 40 C-PLACE1005660//HYPOTHETICAL 64.3 KD GTP-BINDING PROTEIN C02F5.3 IN CHROMOSOME III.//1.90E-
 33//143aa//53%//P34280
 C-PLACE1005669
 C-PLACE1005682//B-CELL LYMPHOMA 3-ENCODED PROTEIN (BCL-3 PROTEIN) //4.90E-09//183aa//33%//
 P20749
 45 C-PLACE1005725//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//7.60E-17//295aa//
 27%//Q11073
 C-PLACE1005736//Human mRNA for BAS-GRIP protein.//0//2378bp//99%//E16311 C-PLACE1005745//ORM1
 PROTEIN.//2.40E-17//137aa//35%//P53224
 C-PLACE1005768
 50 C-PLACE1005815//COLORECTAL MUTANT CANCER PROTEIN (MCC PROTEIN) //1.50E-26//274aa//26%//
 P23508
 C-PLACE1005878//Bovine chlorine channel protein (p64) mRNA, complete cds.//5.90E-137//889bp//85%//L16547
 C-PLACE1005927//HYPOTHETICAL 35.8 KD PROTEIN C12G12.12 IN CHROMOSOME I.//1.60E-38//333aa//
 33%//Q09875
 55 C-PLACE1006071//LAMININ BETA-1 CHAIN PRECURSOR (LAMININ B1 CHAIN) //6.00E-08//215aa//26%//
 P02469
 C-PLACE1006073//Homo sapiens mRNA for glucuronyltransferase I, complete cds.//4.10E-316//1020bp//96%//
 AB009598
 C-PLACE1006079//Homo sapiens distal-less homeobox protein (DLX3) gene, complete cds.//0//1379bp//97%//

AF028233
 C-PLACE1006093
 C-PLACE1006208//Homo sapiens nGAP mRNA, complete cds.//3.30E-151//694bp//100%//AF047711
 C-PLACE1006219//PUTATIVE UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP-
 5 GALACTOSE 4-EPIMERASE).//3.50E-37//302aa//30%//Q57664
 C-PLACE1006277//Homo sapiens mRNA for Z39lg protein.//0//1768bp//99%//AJ132502
 C-PLACE1006290//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-)//8.50E-75//301aa//39%//P43636
 C-PLACE1006443//Homo sapiens PB39 mRNA, complete cds.//4.30E-98//553bp//70%//AF045584
 C-PLACE1006515//Homo sapiens mRNA for KIAA0576 protein, partial cds.//0//2846bp//99%//AB011148
 10 C-PLACE1006716//30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADI-
 POCYTE SPECIFIC PROTEIN ADIPOQ).//4.60E-25//181aa//35%//Q60994
 C-PLACE1006786
 C-PLACE1006809//SLS1.PROTEIN PRECURSOR.//9.10E-10//273aa//27%//P08124
 C-PLACE1006959
 15 C-PLACE1007028//Homo sapiens TDAG51/lp1 homologue 1 (TIH1) mRNA, complete cds.//1.40E-307//1423bp//
 99%//AF151100
 C-PLACE1007040
 C-PLACE1007077//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//2578bp//99%//AB023194
 C-PLACE1007081//COAGULATION FACTOR V PRECURSOR (ACTIVATED PROTEIN C COFACTOR).//5.00E-
 20 20//247aa//34%//Q28107
 C-PLACE1007096//PUTATIVE SUGAR TRANSPORT PROTEIN GUTA.//2.70E-17//174aa//27%//O34368
 C-PLACE1007296//Human mRNA for a presumptive KDEL receptor.//1.10E-185//1038bp//91%//X55885
 C-PLACE1007591
 C-PLACE1007626//Homo sapiens unknown mRNA, complete cds.//3.00E-246//1122bp//99%//AF047439
 25 C-PLACE1007702//Mus musculus TRA1 mRNA, complete cds.//7.50E-41//662bp//64%//D78335
 C-PLACE1007845//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-)//4.80E-14//158aa//40%//P43636
 C-PLACE1007881//HYPOTHETICAL 69.4 KD PROTEIN F13H10.3 IN CHROMOSOME IV.//3.10E-99//504aa//
 42%//Q19425
 C-PLACE1007971
 30 C-PLACE1008282//HEME-REGULATED EUKARYOTIC INITIATION FACTOR EIF-2-ALPHA KINASE (EC 2.7.1.-)
 (HRI).//7.10E-274//627aa//82%//P33279
 C-PLACE1008297//MYOSIN HEAVY CHAIN KINASE B (EC 2.7.1.129) (MHCK B).//1.30E-14//187aa//33%//
 P90648
 C-PLACE1008359//BEM46 PROTEIN (FRAGMENT).//1.70E-50//289aa//42%//P54069
 35 C-PLACE1008469
 C-PLACE1008549//Homo sapiens Ets transcription factor ESE-2b mRNA, complete cds.//0//2274bp//99%//
 AF115403
 C-PLACE1008657//Bovine mRNA for adseverin, complete cds.//7.80E-227//1246bp//90%//D26549
 C-PLACE1008716//Human beta-1,2-N-acetylglucosaminyltransferase II (MGAT2) gene, complete cds.//0//
 40 1888bp//99%//U15128
 C-PLACE1008744//P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
 (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).//4.80E-32//338aa//30%//
 Q01102
 C-PLACE1008984
 45 C-PLACE1008985//Mus musculus synaptotagmin VIII mRNA, partial cds.//3.80E-140//650bp//81%//U20107
 C-PLACE1009067
 C-PLACE1009196
 C-PLACE1009279//cDNA encoding novel physiologically active protein which have serine protease activity.//
 6.60E-86//1414bp//64%//E12965
 50 C-PLACE1009527//Oryctolagus cuniculus mRNA for epithelial calcium channel (ECaC).//1.20E-87//585bp//83%//
 AJ133128
 C-PLACE1009546
 C-PLACE1009600//Mouse mRNA for tetracycline transporter-like protein, complete cds.//1.10E-264//924bp//
 88%//D88315
 55 C-PLACE1009735
 C-PLACE1009982//SALIVARY GILUE PROTEIN SGS-3 PRECURSOR.//5.20E-08//166aa//28%//P02840
 C-PLACE1010011//Homo sapiens AAPT1-like protein mRNA, partial cds.//1.70E-237//1092bp//99%//AF047431
 C-PLACE1010078//ORM1 PROTEIN.//3.70E-19//137aa//37%//P53224

- C-PLACE1010081//Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete cds.//0//2033bp//99%//AF027706
- C-PLACE1010251//FIBRILLIN 2 PRECURSOR.//1.70E-31//201aa//35%//Q61555
- C-PLACE1010445
- 5 C-PLACE1010713//Homo sapiens steroid dehydrogenase homolog mRNA, complete cds.//0//2374bp//99%//AF078850
- C-PLACE1010784//Homo sapiens orphan G protein-coupled receptor (GPR34) gene, complete cds.//2.30E-252//1146bp//99%//AF039686
- 10 C-PLACE1010827//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.90E-19//163aa//34%//P49020
- C-PLACE1010968//PROTEIN-TYROSINE PHOSPHATASE DLAR PRECURSOR (EC 3.1.3.48) (PROTEIN-TYROSINE-PHOSPHATE PHOSPHOHYDROLASE).//3.40E-30//690aa//26%//P16621
- C-PLACE1011045//Homo sapiens E1-like protein mRNA, complete cds.//0//2376bp//99%//AF094516
- 15 C-PLACE1011116//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//3.30E-09//234aa//27%//P08640
- C-PLACE1011181//MSP1 PROTEIN HOMOLOG.//9.40E-82//353aa//47%//P54815
- C-PLACE1011236//Mus musculus mRNA for RST, complete cds.//1.70E-90//1398bp//65%//AB005451
- C-PLACE1011364//MYOTONIN-PROTEIN KINASE (EC 2.7.1.-) (MYOTONIC DYSTROPHY PROTEIN KINASE) (MDPK) (DM-KINASE) (DMK) (DMPK) (MT-PK).//2.20E-09//153aa//32%//Q09013
- 20 C-PLACE1011407//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.80E-133//342aa//59%//Q99676
- C-PLACE1011516//HYPOTHETICAL 21.5 KD PROTEIN IN SEC15-SAP4 INTERGENIC REGION.//1.30E-13//139aa//34%//P53073
- C-PLACE1011708//Homo sapiens intrinsic factor-B12 receptor precursor, mRNA, complete cds.//0//1840bp//98%//AF034611
- 25 C-PLACE1011824//Human Ste20-like kinase (MST2) mRNA, complete cds.//6.40E-202//561bp//92%//U26424
- C-PLACE1011978//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.10E-194//547aa//57%//Q05481
- C-PLACE2000118//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).//3.20E-27//205aa//43%//P70315
- 30 C-PLACE2000219
- C-PLACE3000181//Human protocadherin 42 mRNA, complete cds for abbreviated PC42.//0//2719bp//95%//L11370
- C-PLACE3000213//COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR).//4.60E-68//317aa//34%//P19070
- 35 C-PLACE4000354//COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B RECEPTOR) (CD35 ANTIGEN).//1.00E-129//482aa//29%//P17927
- C-PLACE4000455
- C-SKNMC1000004
- C-SKNMC1000014
- 40 C-SKNMC1000082//BRITTLE-1 PROTEIN PRECURSOR.//3.70E-31//307aa//130%//P29518
- C-THYRO1000036//Homo sapiens collagen alpha 3 type IX (COL9A3) mRNA, complete cds.//1.20E-258//1376bp//93%//L41162
- C-THYRO1000061//Mus musculus mRNA for UBE-1c1, UBE-1c2, UBE-1c3, complete cds.//1.40E-117//1126bp//74%//AB030505
- 45 C-THYRO1000099
- C-THYRO1000196//Homo sapiens Ksp-cadherin (CDH16) mRNA, complete cds.//0//1632bp//91%//AF016272
- C-THYRO1000400//Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 25795.//0//1893bp//99%//AL109665
- C-THYRO1000580//ZINC FINGER PROTEIN 184 (FRAGMENT).//9.90E-114//279aa//59%//Q99676
- 50 C-THYRO1000584//EPIDIDYMIS-SPECIFIC ALPHA-MANNOSIDASE (EC 3.2.1.24) (ALPHA-D-MANNOSIDE MANNOHYDROLASE) (135 KD PROTEIN).//5.40E-127//335aa//71%//Q28949
- C-THYRO1000678//Homo sapiens Cx30 gene.//0//1741bp//97%//AJ005585
- C-THYRO1000776//PROBABLE SULFATE PERMEASE SPBC3H7.02.//1.30E-68//442aa//36%//O74377
- C-THYRO1000795//C.elegans mRNA for Oxoglutarate/malate carrier protein.//8.80E-42//821bp//63%//X76114
- 55 C-THYRO1000846
- C-THYRO1000866//SHK1 KINASE-BINDING PROTEIN 1.//4.40E-91//449aa//44%//P78963
- C-THYRO1000956//Human G protein-coupled receptor APJ gene, complete cds.//0//1583bp//99%//U03642
- C-THYRO1000964//Drosophila melanogaster Pelle associated protein Pellino (Pli) mRNA, complete cds.//1.10E-

- 34//759bp//63%//AF091624
 C-THYRO1000999
 C-THYRO1001063
 5 C-THYRO1001071//GAMMA-ADAPTIN (GOLGI ADAPTOR HA1/AP1 ADAPTIN GAMMA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 GAMMA LARGE CHAIN).//8.20E-14//157aa//33%//P22892
 C-THYRO1001102
 C-THYRO1001113//Homo sapiens mRNA; cDNA DKFZp564E1616 (from clone DKFZp564E1616).//0//1361bp//99%//AL096713
 10 C-THYRO1001128//Homo sapiens mRNA for hypothetical protein (C9orf9 gene).//6.40E-155//648bp//99%//AJ011375
 C-THYRO1001205
 C-THYRO1001237//PHYTOENE DEHYDROGENASE (EC 1.3.-.-) (PHYTOENE DESATURASE) (ALBINO-1 PROTEIN).//3.10E-13//346aa//22%//P21334
 15 C-THYRO1001242//Homo sapiens cleft lip and palate transmembrane protein 1 (CLPTM1) mRNA, complete cds.//0//2468bp//99%//AF037339
 C-THYRO1001266//Human sodium iodide symporter mRNA, complete cds.//7.20E-81//1466bp//62%//U66088
 C-THYRO1001327
 C-THYRO1001456//HYPOTHETICAL 56.2 KD PROTEIN CY31.25C.//9.40E-32//355aa//31%//Q10555
 20 C-THYRO1001457//H.sapiens mRNA for protein kinase C mu.//2.30E-218//1183bp//73%//X75756
 C-THYRO1001471
 C-THYRO1001478//CYTOCHROME B-245 HEAVY CHAIN (P22 PHAGOCYTE B-CYTOCHROME) (NEUTROPHIL CYTOCHROME B, 91 KD POLYPEPTIDE) (CGD91-PHOX) (GP91-PHOX) (CYTOCHROME B(558) BETA CHAIN) (SUPEROXIDE-GENERATING NADPH OXIDASE HEAVY CHAIN SUBUNIT).//8.90E-50//296aa//35%//P04839
 25 C-THYRO1001495
 C-THYRO1001523//Homo sapiens mRNA for TM7XN1 protein.//0//3663bp//99%//AJ011001
 C-THYRO1001529//SERINE PALMITOYLTRANSFERASE 2 (EC 2.3.1.50) (LONG CHAIN BASE BIOSYNTHESIS PROTEIN 2) (SPT 2).//5.50E-25//115aa//53%//Q09925
 30 C-THYRO1001593//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-).//3.10E-203//550aa//62%//P27448
 C-THYRO1001608
 C-THYRO1001641//Homo sapiens CGI-57 protein mRNA, complete cds.//0//1668bp//99%//AF151815
 C-THYRO1001700//SERINE/THREONINE PROTEIN KINASE RIP (EC 2.7.1.-) (CELL DEATH PROTEIN RIP) (RECEPTOR INTERACTING PROTEIN).//9.70E-33//268aa//37%//Q60855
 35 C-THYRO1001702//Mus musculus mRNA for myeloid associated differentiation protein.//1.50E-128//1204bp//73%//AJ001616
 C-THYRO1001725
 C-THYRO1001770//PROBABLE SERINE/THREONINE-PROTEIN KINASE YNL020C (EC 2.7.1.-).//6.30E-20//169aa//35%//P53974
 40 C-THYRO1001803
 C-Y79AA1000030//Homo sapiens mRNA for Fe65L2, complete cds.//0//1828bp//100%//AB018247
 C-Y79AA1000127
 C-Y79AA1000207
 C-Y79AA1000226
 45 C-Y79AA1000270//Bos taurus vacuolar H+ ATPase subunit Ac45 mRNA, complete cds.//1.00E-271//1490bp//83%//U10039
 C-Y79AA1000426//Mus musculus activin beta E subunit mRNA, complete cds.//7.70E-200//1533bp//78%//U96386
 C-Y79AA1000521
 C-Y79AA1000750
 50 C-Y79AA1000776//Mus musculus mRNA for GSG1, complete cds.//2.40E-161//820bp//85%//D87325
 C-Y79AA1000777//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//8.10E-48//283aa//38%//Q00808
 C-Y79AA1000876//PROTEIN DISULHDE ISOMERASE-RELATED PROTEIN PRECURSOR (ERP72).//1.60E-44//210aa//38%//P13667
 55 C-Y79AA1000888//TRNA PSEUDOURIDINE SYNTHASE A (EC 4.2.1.70) (PSEUDOURIDYLATE SYNTHASE I) (PSEUDOURIDINE SYNTHASE I) (URACIL HYDROLYASE).//1.50E-21//267aa//32%//P70973
 C-Y79AA1000959//Homo sapiens Hsp70 binding protein HspBP1 mRNA, complete cds.//4.80E-283//1405bp//95%//AF093420
 C-Y79AA1000967//CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE I (EC 2.7.1.123) (CAM KI-

NASE I).//1.00E-77//359aa//44%//Q14012
 C-Y79AA1001013
 C-Y79AA1001056//Homo sapiens MAID protein mRNA, complete cds.//0//1475bp//99%//AF113535
 C-Y79AA1001062//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, ENDOTHELIAL (B12 PRO-
 5 TEIN).//8.90E-12//132aa//38%//Q13829
 C-Y79AA1001090//NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1)
 (NF-KAPPA-B1 P84/NF-KAPPA-B1 P98)[CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] (FRAG-
 10 MENT).//4.50E-09//144aa//31%//Q63369
 C-Y79AA1001212//Homo sapiens SL15 protein mRNA, complete cds.//6.30E-306//1388bp//99%//AF038961
 C-Y79AA1001264//HYPOTHETICAL 39.9 KD PROTEIN T15H9.1 IN CHROMOSOME II PRECURSOR.//5.10E-
 106//351aa//58%//Q10005
 C-Y79AA1001272//Homo sapiens retinoic acid repressible protein (RARG-1) mRNA, complete cds.//1.50E-183//
 867bp//98%//AF172066
 C-Y79AA1001328//Mus musculus mRNA for Dll3 protein, complete cds.//1.90E-263//1988bp//79%//AB013440
 15 C-Y79AA1001426//ANION EXCHANGE PROTEIN 3 (CARDIAC/BRAIN BAND 3-LIKE PROTEIN) (CAE3/BAE3).//
 6.20E-66//609aa//31%//P48751
 C-Y79AA1001427//Homo sapiens cytochrome b5 reductase 1 (B5R.1) mRNA, complete cds.//0//1588bp//99%//
 AF169481
 C-Y79AA1001430//Homo sapiens mRNA for KIAA0469 protein, complete cds.//0//2943bp//99%//AB007938
 20 C-Y79AA1001523//Homo sapiens transcriptional intermediary factor 1 alpha mRNA, complete cds.//0//2263bp//
 99%//AF119042
 C-Y79AA1001530//Human beta-tubulin gene (5-beta) with ten Alu family members.//0//1920bp//98%//X00734
 C-Y79AA1001592
 C-Y79AA1001727//CELL SURFACE A33 ANTIGEN PRECURSOR.//1.10E-13//286aa//27%//Q99795
 25 C-Y79AA1001787//PROBABLE CALCIUM-TRANSPORTING ATPASE 9 (EC 3.6.1.38).//1.70E-133//544aa//37%//
 Q12697
 C-Y79AA1001793//Mus musculus mRNA for GSG1, complete cds.//3.70E-126//532bp//78%//D87325
 C-Y79AA1001795//Homo sapiens mRNA for GalT4 protein.//2.30E-250//1137bp//99%//Y15061
 C-Y79AA1001799//MITOCHONDRIAL RNA SPLICING PROTEIN MSR4.//3.40E-54//182aa//39%//P23500
 30 C-Y79AA1001803//Homo sapiens secretogranin III mRNA, complete cds.//0//1871bp//99%//AF078851
 C-Y79AA1001863
 C-Y79AA1002022//POLIOVIRUS RECEPTOR HOMOLOG PRECURSOR.//2.20E-06//140aa//26%//P32507
 C-Y79AA1002058//Mus musculus Gng3lg mRNA, complete cds.//4.10E-167//1145bp//83%//AF069954
 C-Y79AA1002121//HISTONE H1.//4.90E-12//114aa//35%//P35060
 35 C-Y79AA1002129
 C-Y79AA1002213//HYPOTHETICAL 52.7 KD PROTEIN C38C10.2 IN CHROMOSOME III.//1.20E-98//262aa//
 41%//Q03567
 C-Y79AA1002334//GLUCOSE REPRESSION MEDIATOR PROTEIN.//1.70E-10//333aa//23%//P14922
 C-Y79AA1002373//Mus musculus mRNA for GSG1, complete cds.//7.20E-147//680bp//79%//D87325
 40 C-Y79AA1002376//Rattus norvegicus cytoplasmic dynein intermediate chain 2B mRNA, complete cds.//1.50E-
 304//1667bp//90%//U39045
 C-Y79AA1002378//Homo sapiens zinc finger protein NY-REN-21 antigen mRNA, partial cds.//0//963bp//99%//
 AF155100
 C-Y79AA1002381//Homo sapiens cell cycle related kinase mRNA, complete cds.//0//1791bp//98%//AF035013
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Claims

1. Use of an oligonucleotide as a primer for synthesizing the polynucleotide comprising the nucleotide sequence set
 50 forth in any one of SEQ ID NOs: 1-829 and 2545, or the complementary strand thereof, wherein said oligonucleotide
 is complementary to said polynucleotide or the complementary strand thereof and comprises at least 15 nucle-
 otides.
2. A primer set for synthesizing polynucleotides, the primer set comprising an oligo-dT primer and an oligonucleotide
 55 complementary to the complementary strand of the polynucleotide comprising the nucleotide sequence set forth
 in any one of SEQ ID NOs: 1-829 and 2545, wherein said oligonucleotide comprises at least 15 nucleotides.
3. A primer set for synthesizing polynucleotides, the primer set comprising a combination of an oligonucleotide com-

prising a nucleotide sequence complementary to the complementary strand of the polynucleotide comprising a 5'-end nucleotide sequence and an oligonucleotide comprising a nucleotide sequence complementary to the polynucleotide comprising a 3'-end nucleotide sequence, wherein said oligonucleotides comprise at least 15 nucleotides and wherein said combination of 5'-end nucleotide sequence.3'-end nucleotide sequence is selected from the group consisting of:

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4. A polynucleotide which can be synthesized with the primer set of claim 2 or 3.
5. A polynucleotide comprising a coding region in the polynucleotide of claim 4.
6. A substantially pure protein encoded by polynucleotide of claim 4.
7. A partial peptide of the protein of claim 6.
8. An isolated polynucleotide selected from the group consisting of
 - (a) a polynucleotide comprising a coding region of the nucleotide sequence set forth in any one of the following SEQ ID NOs:

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(b) a polynucleotide comprising a nucleotide sequence encoding a protein comprising the amino acid sequence

EP 1 130 094 A2

set forth in any one of the following SEQ ID NOs:

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- (c) a polynucleotide comprising a nucleotide sequence encoding a protein comprising an amino acid sequence selected from the amino acid sequences of (b), in which one or more amino acids are substituted, deleted, inserted, and/or added, wherein said protein is functionally equivalent to the protein comprising said amino acid sequence selected from the amino acid sequences of (b);
 - (d) a polynucleotide that hybridizes with a polynucleotide comprising a nucleotide sequence selected from the nucleotide sequences of (a), and that comprises a nucleotide sequence encoding a protein functionally equivalent to the protein encoded by the nucleotide sequence selected from the nucleotide sequences of (a);
 - (e) a polynucleotide comprising a nucleotide sequence encoding a partial amino acid sequence of a protein encoded by the polynucleotide of (a) to (d);
 - (f) a polynucleotide comprising a nucleotide sequence with at least 70% identity to the nucleotide sequence of (a).
9. A substantially pure protein encoded by the polynucleotide of claim 8.
 10. An antibody against the protein or peptide of any one of claims 6, 7, and 9.
 11. A vector comprising the polynucleotide of claim 5 or 8.
 12. A transformant carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.
 13. A transformant expressively carrying the polynucleotide of claim 5 or 8, or the vector of claim 11.
 14. A method for producing the protein or peptide of any one of claims 6, 7, and 9, comprising culturing the transformant of claim 13 and recovering the expression product.
 15. An oligonucleotide comprising the nucleotide sequence of claim 8 (a) or the nucleotide sequence complementary to the complementary strand thereof, wherein said oligonucleotide comprises 15 nucleotides or more.
 16. Use of the oligonucleotide of claim 15 as a primer for synthesizing a polynucleotide.
 17. Use of the oligonucleotide of claim 15 as a probe for detecting a gene.
 18. An antisense polynucleotide against the polynucleotide of claim 8, or the portion thereof.
 19. A method for synthesizing a polynucleotide, the method comprising:
 - a) synthesizing a complementary strand using a cDNA library as a template, and using the primer set of claim 2 or 3, or the primer of claim 16; and
 - b) recovering the synthesized product.
 20. The method of claim 19, wherein the cDNA library is obtainable by oligo-capping method.
 21. The method of claim 19, wherein the complementary strand is obtainable by PCR.
 22. A method for detecting the polynucleotide of claim 8, the method comprising:
 - a) incubating a target polynucleotide with the oligonucleotide of claim 15 under the conditions where hybridization occurs, and
 - b) detecting the hybridization of the target polynucleotide with the oligonucleotide of claim 15.
 23. A database of polynucleotides and/or proteins, the database comprising information on at least one sequence selected from the nucleotide sequences of claim 8 (a) and/or the amino acid sequences of claim 8 (b), or a medium

on which the database is stored.

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Figure 1

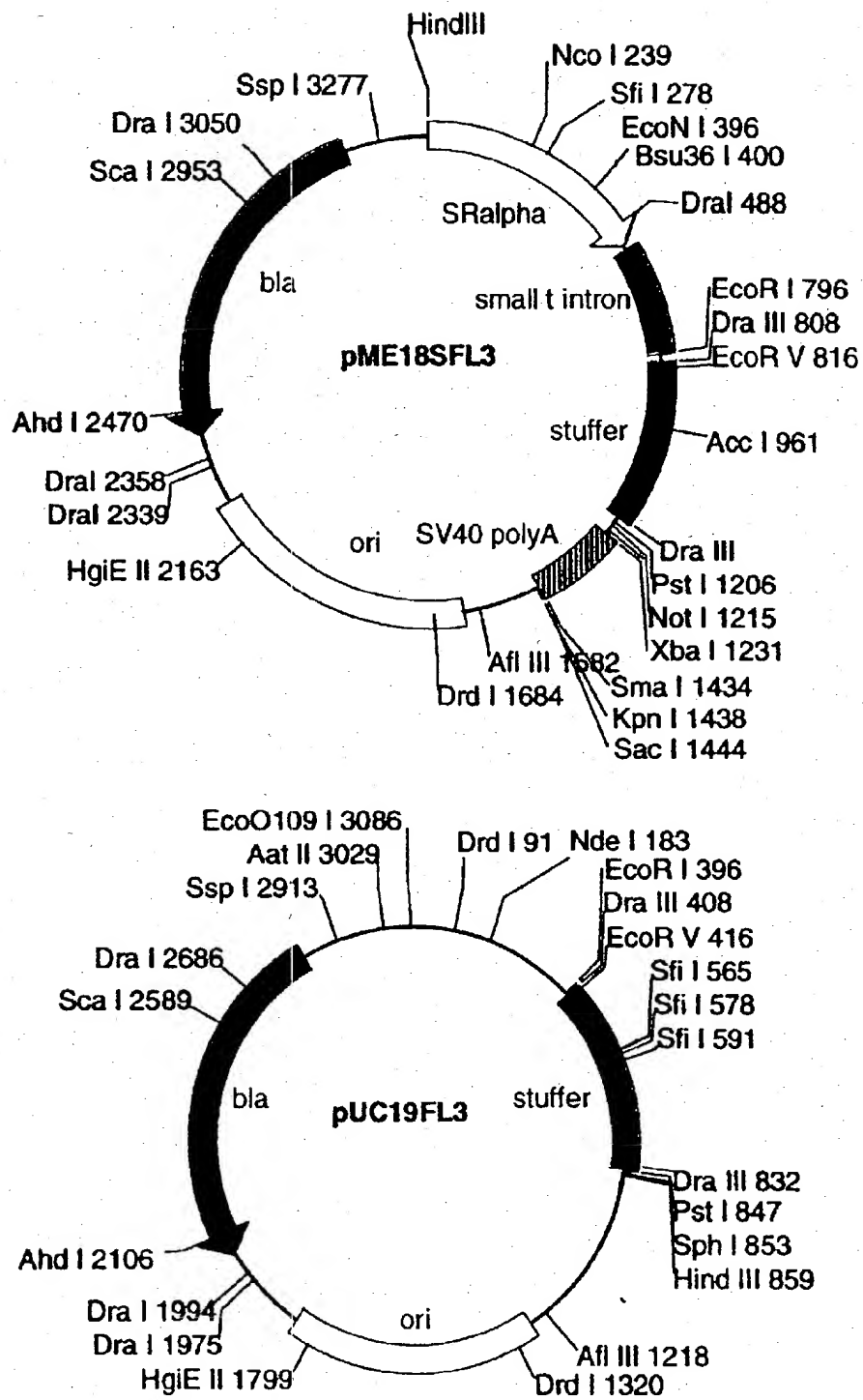


Figure 2

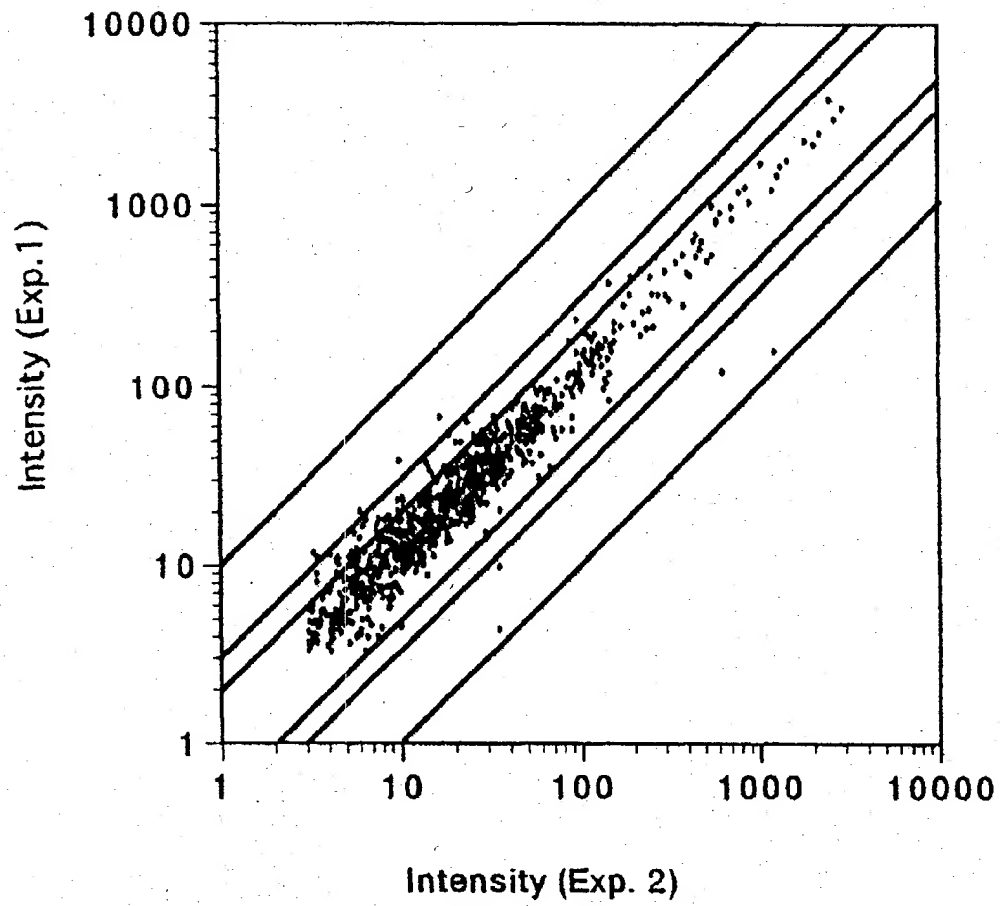
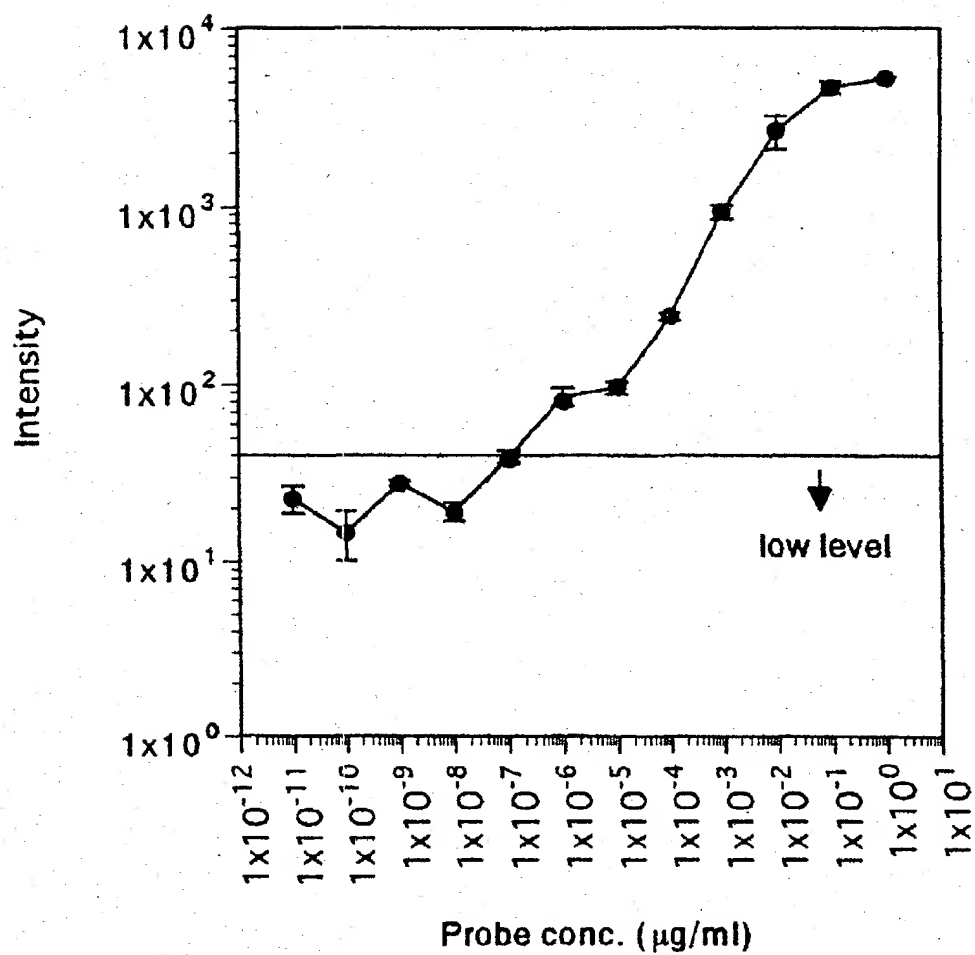


Figure 3



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